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OM protein - protein search, using sw model

Run on: August 19, 2005, 10:50:49 ; Search time 22 Seconds
(without alignments)
81.435 Million cell upd

Title: US-09-846-328B-1 COPY 2 25

Perfect score: 123

Sequence: 1 DAHKSEVAHRFKDLGEENFKALVL 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Minimum DB seq length:	200000000
Maximum DB seq length:	2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Database :
Issued Patents: AA.*
1: /cgn2_6/pdata/1/iaa/5A_COMB pep.*
2: /cgn2_6/pdata/1/iaa/5B_COMB pep.*
3: /cgn2_6/pdata/1/iaa/6A_COMB pep.*
4: /cgn2_6/pdata/1/iaa/6B_COMB pep.*
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6: /cgn2_6/pdata/1/iaa/backfiles1.pe

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	123	100.0	28	4	US-09-846-329A-1	Sequence 1, Appli
2	123	100.0	585	1	US-08-153-799-14	Sequence 14, Appl
3	123	100.0	585	1	US-08-448-196A-3	Sequence 3, Appli
4	123	100.0	585	2	US-08-984-176-1	Sequence 1, Appli
5	123	100.0	585	2	US-08-702-572-2	Sequence 2, Appli
6	123	100.0	585	3	US-08-769-746-2	Sequence 2, Appli
7	123	100.0	609	1	US-08-222-619-3	Sequence 3, Appli
8	123	100.0	609	1	US-08-433-037-4	Sequence 4, Appli
9	123	100.0	609	4	US-08-897-956A-2	Sequence 2, Appli
10	123	100.0	609	4	US-09-376-594A-977	Sequence 977, App
11	123	100.0	609	4	US-09-819-039-370	Sequence 370, App
12	123	100.0	609	5	PCT-US95-04075-3	Sequence 3, Appli
13	123	100.0	610	2	US-08-797-689-2	Sequence 2, Appli
14	123	100.0	610	4	US-09-984-186-2	Sequence 2, Appli
15	123	100.0	622	4	US-09-949-016-1170	Sequence 1170, A
16	123	100.0	783	1	US-08-256-938-2	Sequence 2, Appli
17	123	100.0	787	1	US-08-256-938-4	Sequence 4, Appli
18	123	100.0	787	2	US-08-797-689-16	Sequence 16, Appl
19	123	100.0	787	4	US-09-984-186-16	Sequence 16, Appl
20	123	100.0	978	4	US-08-897-956A-3	Sequence 3, Appli
21	109	88.6	582	1	US-08-134-638-1	Sequence 1, Appli
22	109	88.6	583	1	US-08-448-196A-4	Sequence 4, Appli
23	105	86.2	584	1	US-08-448-196A-7	Sequence 7, Appli
24	105	85.4	583	1	US-08-448-196A-6	Sequence 6, Appli
25	100	81.3	583	1	US-08-448-196A-5	Sequence 5, Appli
26	74	60.2	15	4	US-09-845-764A-1	Sequence 1, Appli
27	70	56.9	17	1	US-08-470-187-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

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US-09-846-329A-1
; Sequence 1, Application US/09846329A
; Patent No. 6620786
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: Biopolymer Marker Indication
; TITLE OF INVENTION: of 2937 Daltons
; FILE REFERENCE: 2132.052
; CURRENT APPLICATION NUMBER: US/09/846, 329A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-846-329A-1

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Query Match 100.0%; Score 123; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 5.6e-13;
Matches 24; Conservative 0; Mismatches 0 Indels

QY	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
QY	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24
DB	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

RESULT 2

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US-08-153-799-14
; Sequence 14, Application US/08153799
; Patent No. 5766883
; GENERAL INFORMATION:
;
; APPLICANT: Ballance, David J
; APPLICANT: Goodey, Andrew R
; TITLE OF INVENTION: Polypeptides
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: R Hain Swope, BOC Health Care Inc
; STREET: 100 Mountain Avenue
; CITY: Murray Hill
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07974
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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```
;
; ADDRESSEE: Centeon L.L.C.
; STREET: 1020 First Avenue
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702.572
; FILING DATE: 11-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 95/23857
; FILING DATE: 1-MAR-1995
; APPLICATION NUMBER: GB 9404270.2
; FILING DATE: 5-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Naomi Blawas
; REGISTRATION NUMBER: 38,384
; REFERENCE/DOCKET NUMBER: CB0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610/878/4294
; TELEFAX: 610/878/4221
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-702-572-2
;
; Query Match 100.0%; Score 123; DB 2; Length 585;
; Best Local Similarity 100.0%; Pred. No. 1.9e-11;
; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 DAHKSEVAHRFKDLGEENFKALVL 24
; Db 1 DAHKSEVAHRFKDLGEENFKALVL 24
;
; RESULT 6
; US-08-769-746-2
; Sequence 2, Application US/08769746
; Patent No. 6274305
; GENERAL INFORMATION:
; APPLICANT: Sonnenschein, Carlos
; APPLICANT: Soto, Ana M.
; TITLE OF INVENTION: Inhibiting Proliferation of Cancer Cells
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Medlen & Carroll, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: California
; COUNTRY: United States of America
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/769,746
; FILING DATE: 19-DEC-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Carroll, Peter G.
; REGISTRATION NUMBER: 32,837
; REFERENCE/DOCKET NUMBER: MBRI-02584
;
; ADDRESS: Centeon L.L.C.
; STREET: 1020 First Avenue
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702.572
; FILING DATE: 11-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO 95/23857
; FILING DATE: 1-MAR-1995
; APPLICATION NUMBER: GB 9404270.2
; FILING DATE: 5-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Naomi Blawas
; REGISTRATION NUMBER: 38,384
; REFERENCE/DOCKET NUMBER: CB0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610/878/4294
; TELEFAX: 610/878/4221
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 585 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-702-572-2
;
; Query Match 100.0%; Score 123; DB 2; Length 585;
; Best Local Similarity 100.0%; Pred. No. 1.9e-11;
; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 DAHKSEVAHRFKDLGEENFKALVL 24
; Db 1 DAHKSEVAHRFKDLGEENFKALVL 24
;
; RESULT 7
; US-08-222-619-3
; Sequence 3, Application US/08222619
; Patent No. 5652352
; GENERAL INFORMATION:
; APPLICANT: Lichenstein, Henri
; APPLICANT: Lyons, David
; APPLICANT: Wurfel, Mark
; APPLICANT: Wright, Samuel
; TITLE OF INVENTION: Afamin: A Human Serum Albumin-Like
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Center, Patent Operations/RRC
; STREET: 1840 DeHavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,619
; FILING DATE:
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 609 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-222-619-3
;
; Query Match 100.0%; Score 123; DB 1; Length 609;
; Best Local Similarity 100.0%; Pred. No. 2e-11;
; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 DAHKSEVAHRFKDLGEENFKALVL 24
; Db 25 DAHKSEVAHRFKDLGEENFKALVL 48
;
; RESULT 8
; US-08-433-037-4
; Sequence 4, Application US/08433037
; Patent No. 5707828
; GENERAL INFORMATION:
; APPLICANT: Sreekrishna, Kotikanyadan
; APPLICANT: Barr, Kathryn A.
```

APPLICANT: Brierley, Russell A.
APPLICANT: Thill, Gregory P.
APPLICANT: Tschoep, Juerg F.
TITLE OF INVENTION: EXPRESSION OF HUMAN SERUM ALBUMIN IN
TITLE OF INVENTION: PICHIA PASTORIS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/433,037
FILING DATE: 03-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9108Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 609 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-433-037-4

Query Match 100.0%; Score 123; DB 1; Length 609;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKEVAHRFKDLGEENFKALVL 24
Db 25 DAHKEVAHRFKDLGEENFKALVL 48

RESULT 9
US-08-897-956A-2
Sequence 2, Application US/08897956A
Patent No. 6423512
GENERAL INFORMATION:
APPLICANT: Mary Ellen Digan
APPLICANT: Philip Lake
APPLICANT: Hermann Gram
TITLE OF INVENTION: Fusion Polypeptides
FILE REFERENCE: 600-7244/CPA
CURRENT APPLICATION NUMBER: US/08/897,956A
CURRENT FILING DATE: 1997-07-21
PRIOR APPLICATION NUMBER: 60/022,689
PRIOR FILING DATE: 1996-07-26
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 609
TYPE: PRT
ORGANISM: Homo Sapiens
US-08-897-956A-2

Query Match 100.0%; Score 123; DB 4; Length 609;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKEVAHRFKDLGEENFKALVL 24
Db 25 DAHKEVAHRFKDLGEENFKALVL 48

RESULT 10
US-09-976-594-977
Sequence 977, Application US/09976594
Patent No. 6673549
GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 977
LENGTH: 609
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6673549 088957CD1
US-09-976-594-977

Query Match 100.0%; Score 123; DB 4; Length 609;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKEVAHRFKDLGEENFKALVL 24
Db 25 DAHKEVAHRFKDLGEENFKALVL 48

RESULT 11
US-09-919-039-370
Sequence 370, Application US/09919039
Patent No. 6727066
GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
SEQ ID NO 370
LENGTH: 609
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6727066 088957CD1
US-09-919-039-370

Query Match 100.0%; Score 123; DB 4; Length 609;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKEVAHRFKDLGEENFKALVL 24
Db 25 DAHKEVAHRFKDLGEENFKALVL 48

RESULT 12
PCT-US95-04075-3
Sequence 3, Application PC/TUS9504075


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;
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 610 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-984-186--2

Query Match      100.0%; Score 123; DB 4; Length 610;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAKHSEVAHRFKDLGEENFKALVL 24
    |||||
Db 25 DAKHSEVAHRFKDLGEENFKALVL 48

RESULT 15
US-09-949-016-11170
; Sequence 11170, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11170
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11170

Query Match      100.0%; Score 123; DB 4; Length 622;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAKHSEVAHRFKDLGEENFKALVL 24
    |||||
Db 38 DAKHSEVAHRFKDLGEENFKALVL 61

RESULT 16
US-08-256-938-2
; Sequence 2, Application US/08256938
; Patent No. 5665863
; GENERAL INFORMATION:
; APPLICANT: Yeh, Patrice
; TITLE OF INVENTION: NEW POLYPEPTIDES HAVING GRANULOCYTE
; COLONY STIMULATING ACTIVITY, PREPARATION THEREOF AND
; USES THEREOF
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING SAID POLYPEPTIDES
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Word 5.0 (PatentIn)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,938
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 92/01065
; FILING DATE: 31-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Goodman, Rosanne
; REGISTRATION NUMBER: 32,534
; REFERENCE/DOCKET NUMBER: ST92007-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-3817
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 787 amino acids
; TYPE: amino acid
; COMPUTER: Macintosh
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Qy	1	DAKSEVAHRRFKOLGEENFKALVL	24
Qy			
pb	203	DAKSEVAHRRFKOLGEENFKALVL	226

;; COUNTRY: USA
;; ZIP: 35812
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/448,196A
;; FILING DATE: 23-MAY-1995
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BROAD JR., ROBERT L.
;; REGISTRATION NUMBER: 18,757
;; REFERENCE/DOCKET NUMBER: XX/MFS-28402-2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 205-544-0021
;; TELEFAX: 205-544-0258
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 584 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
;; US-08-448-196A-7

Query Match 86.2%; Score 106; DB 1; Length 584;
Best Local Similarity 79.2%; Pred. No. 9.9e-09;
Matches 19; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGEENFKALVL 24
|:||||:|||||:|||||:
Db 1 EAHKSEIAHRFNDLGEQHKGLVL 24

RESULT 24
US-08-448-196A-6
; Sequence 6, Application US/08448196A
; Patent No. 5780594
; GENERAL INFORMATION:
; APPLICANT: CARTER, DANIEL C.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS
; TITLE OF INVENTION: CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR
; TITLE OF INVENTION: CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NASA
; STREET: MARSHALL SPACE FLIGHT CENTER
; CITY: HUNTSVILLE
; STATE: ALABAMA
; COUNTRY: USA
; ZIP: 35812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,196A
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: BROAD JR., ROBERT L.
; REGISTRATION NUMBER: 18,757
; REFERENCE/DOCKET NUMBER: XX/MFS-28402-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 205-544-0021
; TELEFAX: 205-544-0258
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:

;; LENGTH: 583 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; FRAGMENT TYPE: N-terminal
;; US-08-448-196A-6

Query Match 85.4%; Score 105; DB 1; Length 583;
Best Local Similarity 79.2%; Pred. No. 1.4e-08;
Matches 19; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGEENFKALVL 24
|:||||:|||||:|||||:
Db 1 DTHKSEIAHRFNDLGEENFQGLVL 24

RESULT 25
US-08-448-196A-5
; Sequence 5, Application US/08448196A
; Patent No. 5780594
; GENERAL INFORMATION:
; APPLICANT: CARTER, DANIEL C.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN FRAGMENTS
; TITLE OF INVENTION: CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR
; TITLE OF INVENTION: CONTAINING SPECIFIC BINDING REGIONS OF SERUM ALBUMIN OR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NASA
; STREET: MARSHALL SPACE FLIGHT CENTER
; CITY: HUNTSVILLE
; STATE: ALABAMA
; COUNTRY: USA
; ZIP: 35812
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,196A
; FILING DATE: 23-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: BROAD JR., ROBERT L.
; REGISTRATION NUMBER: 18,757
; REFERENCE/DOCKET NUMBER: XX/MFS-28402-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 205-544-0021
; TELEFAX: 205-544-0258
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 583 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; US-08-448-196A-5

Query Match 81.3%; Score 100; DB 1; Length 583;
Best Local Similarity 75.0%; Pred. No. 9.1e-08;
Matches 18; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGEENFKALVL 24
|:||||:|||||:|||||:
Db 1 DTHKSEIAHRFNDLGEQHKGLVL 24

RESULT 26
US-09-845-764A-1

; Sequence 1, Application US/09845764A
; Patent No. 6693080
; GENERAL INFORMATION:
; APPLICANT: Jackowski, George
; TITLE OF INVENTION: BIOPOLYMER MARKER INDICATIVE OF DISEASE STATE HAVING A MOLECULAR
; FILE REFERENCE: 2132.037
; CURRENT APPLICATION NUMBER: US/09/845,764A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-845-764A-1

Query Match 60.2%; Score 74; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFKDL 14
|||||
Db 2 DAHKSEVAHRFKDL 15

RESULT 27
US-08-470-187-1
; Sequence 1, Application US/08470187
; Patent No. 5532152
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine E.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,187
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5532152and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-470-187-1

Query Match 60.2%; Score 74; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFKDL 14
|||||
Db 2 DAHKSEVAHRFKDL 15

RESULT 27
US-08-470-187-1
; Sequence 1, Application US/08470187
; Patent No. 5532152
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine E.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,187
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5532152and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-470-187-1

Query Match 56.9%; Score 70; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FKDLGEENFKALVL 24
|||||
Db 1 FKDLGEENFKALVL 14

RESULT 28
US-08-318-905-1
; Sequence 1, Application US/08318905
; Patent No. 5641669
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,905
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 6-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5641669and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32205
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-318-905-1

Query Match 56.9%; Score 70; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 FKDLGEENFKALVL 24
|||||
Db 1 FKDLGEENFKALVL 14

RESULT 29
US-08-483-232-1
; Sequence 1, Application US/08483232
; Patent No. 5656431
; GENERAL INFORMATION:

APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,232
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 565643land, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32689
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-483-232-1
Query Match 56.9%; Score 70; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 FKDLGEENFKALVL 24
Db 1 FKDLGEENFKALVL 14
RESULT 30
US-08-483-140-1
Sequence 1, Application US/08483140
Patent No. 5698403
GENERAL INFORMATION:
APPLICANT: ICOS Corporation
TITLE OF INVENTION: Platelet-Activating Factor Acetyl
TITLE OF INVENTION: Hydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,140
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 6-OCT-1994
APPLICATION NUMBER: US 08/133,803
FILING DATE: 6-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5698403and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32781
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-483-140-1
Query Match 56.9%; Score 70; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 11 FKDLGEENFKALVL 24
Db 1 FKDLGEENFKALVL 14
RESULT 31
US-08-485-938A-1
Sequence 1, Application US/08485938A
Patent No. 5847088
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,938A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:

```
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5847088and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-485-938A-1

Query Match 56.9%; Score 70; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 FKDLGEENFKALVL 24
Db 1 FKDLGEENFKALVL 14

RESULT 32
US-08-910-041-1
; Sequence 1, Application US/08910041
; Patent No. 5977308
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,041
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,232
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 35,547
; REFERENCE/DOCKET NUMBER: 27866/34026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
```

```
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-910-041-1

Query Match 56.9%; Score 70; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 FKDLGEENFKALVL 24
Db 1 FKDLGEENFKALVL 14

RESULT 33
US-09-328-474-1
; Sequence 1, Application US/09328474
; Patent No. 6045794
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/328,474
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,232
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27866/34026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-328-474-1
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Query Match 56.9%; Score 70; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 FKDLGEENFKALVL 24
Db 1 FKDLGEENFKALVL 14

RESULT 34

US-09-100-546-1
; Sequence 1, Application US/09100546
; Patent No. 6099836
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,546
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,715
; FILING DATE:
; FILING DATE:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6099836and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32793
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-546-1

Query Match 56.9%; Score 70; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 FKDLGEENFKALVL 24
Db 1 FKDLGEENFKALVL 14

RESULT 35

US-09-010-715-1
; Sequence 1, Application US/09010715
; Patent No. 6146625
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,715
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6146625and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32793
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-010-715-1

Query Match 56.9%; Score 70; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 FKDLGEENFKALVL 24
Db 1 FKDLGEENFKALVL 14

RESULT 36

US-09-577-758-1
; Sequence 1, Application US/09577758
; Patent No. 6203790
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S. D.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase

```

, NUMBER OF SEQUENCES: 30
, CORRESPONDENCE ADDRESS:
, ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
, STREET: 6300 Sears Tower, 233 South Wacker Drive
, CITY: Chicago
, STATE: Illinois
, COUNTRY: United States of America
, ZIP: 60606-6402
, COMPUTER READABLE FORM:
, MEDIUM TYPE: Floppy disk
, COMPUTER: IBM PC compatible
, OPERATING SYSTEM: PC-DOS/MS-DOS
, SOFTWARE: PatentIn Release #1.0, Version #1.25
, CURRENT APPLICATION DATA: US/09/577,758
, FILING DATE:
, CLASSIFICATION:
, PRIOR APPLICATION DATA:
, APPLICATION NUMBER: 09/010,715
, FILING DATE:
, APPLICATION DATA:
, APPLICATION NUMBER: US 08/133,803
, FILING DATE: 06-OCT-1993
, ATTORNEY/AGENT INFORMATION:
, NAME: No. 6203790and, Greta E.
, REGISTRATION NUMBER: 35,302
, REFERENCE/DOCKET NUMBER: 27866/32793
, TELECOMMUNICATION INFORMATION:
, TELEPHONE: (312) 474-6300
, TELEFAX: (312) 474-0448
, TELEX: 25-3658
, INFORMATION FOR SEQ ID NO: 1:
, SEQUENCE CHARACTERISTICS:
, LENGTH: 17 amino acids
, TYPE: amino acid
, TOPOLOGY: linear
, MOLECULE TYPE: peptide
, US-09-577-758-1

```

Query Match 56.9%; Score 70; DB 3; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 14; Conservative 0; Mismatches 0; Indels

Qy 11 FKDLGEENFKALVL 24
 |||||
Db 1 FKDLGEENFKALVL 14

RESULT 37
US-08-803-364-7
; Sequence 7, Application US/08803364
; Patent No. 5864014
; GENERAL INFORMATION:
; APPLICANT: FASANO, Alessio
; TITLE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MIION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
; CITY: Washington, D.C.
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,364
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/_____
 FILING DATE: 20 FEB 1997
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: KIT, Gordon
 REGISTRATION NUMBER: 30,764
 REFERENCE/DOCKET NUMBER: A-6888
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 293-7060
 TELEFAX: (202) 293-7860
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 US-08-803-364-7

Query Match 55.3%; Score 68; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 13; Conservative 0; Mismatches 0; Indels

Qy	2	AHKSEVAHRFKDL	14
D _b	1	AHKSEVAHRFKDL	13

```

1 RESULT 38
2 US-09-024-198-13
3 ; Sequence 13, Application US/09024198
4 ; Patent No. 5912323
5 ; GENERAL INFORMATION:
6 ; APPLICANT: FASANO, Alessio
7 ; TITLE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR
8 ; NUMBER OF SEQUENCES: 18
9 ; CORRESPONDENCE ADDRESS:
10 ADDRESSEE: SUGHRUE, MIOM, ZINN, MACPEAK & SEAS
11 STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
12 City: Washington, D.C.
13 STATE: D.C.
14 COUNTRY: U.S.A.
15 ZIP: 20037
16 ; COMPUTER READABLE FORM:
17 ; MEDIUM TYPE: Floppy disk
18 ; COMPUTER: IBM PC compatible
19 ; OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: Patent In Release #1.0, Version #1.25
21 ; CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/09/024,198
23 FILING DATE: 17 FEB 1998

```

Query Match 55.3%; Score 68; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AHKSEVAHRFKDL 14
Db 1 AHKSEVAHRFKDL 13

RESULT 39
US-09-186-409-13
; Sequence 13, Application US/09186409
; Patent No. 5948629
; GENERAL INFORMATION:
; APPLICANT: FASANO, Alessio
; TITLE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
; CITY: Washington, D.C.
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/186.409
; FILING DATE: 5 NOV 1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/024,198
; FILING DATE: 17 FEB 1998

CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/803,364
; FILING DATE: 20 FEB 1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KIT, Gordon
; REGISTRATION NUMBER: 30,764
; REFERENCE/DOCKET NUMBER: A-7306
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-09-186-409-13

Query Match 55.3%; Score 68; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AHKSEVAHRFKDL 14
Db 1 AHKSEVAHRFKDL 13

RESULT 40
US-08-803-364-1
; Sequence 1, Application US/08803364
; Patent No. 5864014
; GENERAL INFORMATION:
; APPLICANT: FASANO, Alessio
; TITLE OF INVENTION: ZONULA OCCLUDENS TOXIN RECEPTOR
; NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
; CITY: Washington, D.C.
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/803,364
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: 08/____, ____
; APPLICATION NUMBER:
; FILING DATE: 20 FEB 1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: KIT, Gordon
; REGISTRATION NUMBER: 30,764
; REFERENCE/DOCKET NUMBER: A-6888
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-08-803-364-1

Query Match 51.2%; Score 63; DB 2; Length 16;
Best Local Similarity 85.7%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 HKSEVAHRFKDLGE 16
Db 3 HKSEVAHRFKDLQE 16

Search completed: August 19, 2005, 10:59:14
Job time : 24 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 19, 2005, 10:48:50 ; Search time 163 Seconds
(without alignments)
56.946 Million cell updates/sec

Title: US-09-846-328b-1_COPY_2_25

Perfect score: 123

Sequence: 1 DAHKEVAHRFKDLGEENFALVL 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_l6Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	123	100.0	26	6	ABU08846 Serum alb
2	123	100.0	26	6	ABG75942 Human ser
3	123	100.0	28	6	ABU08847 Serum alb
4	123	100.0	28	6	ABU09223 Serum alb
5	123	100.0	116	4	AAO02642 Human pol
6	123	100.0	119	4	AAO11632 Human pol
7	123	100.0	133	1	AAP30004 Sequence
8	123	100.0	192	4	AAP29875 Novel hum
9	123	100.0	195	5	AAU29875 Novel hum
10	123	100.0	195	7	AAU17048 Human ser
11	123	100.0	204	3	ABU10022 Human ser
12	123	100.0	214	4	AAU83947 Yeast cod
13	123	100.0	214	4	AAU29874 Novel hum
14	123	100.0	236	5	AAU17051 Human alb
15	123	100.0	241	5	AAU16984 Alpha-MSH
16	123	100.0	241	7	ABU10025 Alpha-MSH
17	123	100.0	242	5	AAU16985 Alpha-MSH
18	123	100.0	244	5	AAU16986 Alpha-MSH
19	123	100.0	245	5	AAU16987 Alpha-MSH
20	123	100.0	245	5	AAU16988 Alpha-MSH
21	123	100.0	268	7	ABU10026 Alpha-MSH
22	123	100.0	289	4	AAU29581 Novel hum
23	123	100.0	289	4	AAU29575 Novel hum
24	123	100.0	303	2	AAU14178 Human ser
25	123	100.0	373	1	AAP90387 N-termina

26	123	100.0	388	1	AAP90389 N-termina
27	123	100.0	389	1	AAP90390 N-termina
28	123	100.0	390	1	AAP90391 N-termina
29	123	100.0	401	4	AAU29876 Novel hum
30	123	100.0	407	1	AAP90392 N-termina
31	123	100.0	500	7	ADD32019 Heterolog
32	123	100.0	544	8	ABM84998 Human dia
33	123	100.0	550	4	AAU29877 Novel hum
34	123	100.0	571	8	ABM84997 Human dia
35	123	100.0	573	8	ABM84996 Human dia
36	123	100.0	573	8	ABM84995 Human dia
37	123	100.0	584	6	ABG72381 Mature hu
38	123	100.0	585	1	AAP93344 Sequence
39	123	100.0	585	1	AAP90388 Mature hu
40	123	100.0	585	1	AAP91422 Human nor
41	123	100.0	585	2	AAR05318 Human ser
42	123	100.0	585	2	AAR08457 Human ser
43	123	100.0	585	2	AAR26207 Human ser
44	123	100.0	585	2	AAR26362 Synthetic
45	123	100.0	585	2	AAR20029 Human ser

ALIGNMENTS

RESULT 1
ABU08846
ID ABU08846 standard; peptide; 26 AA.
XX
AC ABU08846;
XX
DT 25-AUG-2003 (first entry)
XX
DE Serum albumin peptide, #3, used for physiological condition diagnostics.
XX
KW Proteomic; human; physiological condition; analyte; biopolymer;
KW biomarker; serum albumin; insulin resistance.
XX
OS Homo sapiens.
XX
PN US2002160420-A1.
XX
PD 31-OCT-2002.
XX
PF 30-APR-2001; 2001US-00846330.
XX
PR 30-APR-2001; 2001US-00846330.
XX
(JACK/) JACKOWSKI G.
(THAT/) THATCHER B.
(WARS/) MARSHALL J.
(YANT/) YANTHA J.
(VREE/) VREES T.
Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;
WPI; 2003-491923/46.
Determining proteomic basis e.g. basis for diagnosing existence of or predicting development and/or progression of abnormal physiological conditions based upon the presence of proteomic materials.
Disclosure; Page 22; 25pp; English.

The invention discloses a method for determining a proteomic basis for development and progression of abnormal physiological conditions. The method comprises isolating one or more patient specific proteomic materials from a sample and comparing it against a library of proteomic materials having characteristics identifiable with both normal and abnormal physiological conditions or their predictive hallmarks. The method is useful for determining a proteomic basis for development and progression of abnormal physiological conditions. The method is also useful for evaluating samples containing several analytes/biopolymers for

CC the presence of physiological condition specific sequences. The peptide
CC presented is a biomarker from serum albumin and is associated with
CC insulin resistance
XX
SQ Sequence 26 AA;

Query Match 100.0%; Score 123; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.6e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFKDLGEENFKALVL 24
DB 2 DAHKSEVAHRFKDLGEENFKALVL 25
|||||

RESULT 2
ABG75942
ID ABG75942 standard; peptide; 26 AA.
XX
AC ABG75942;
XX
DT 08-MAY-2003 (first entry)
XX
DE Human serum albumin biopolymer marker peptide.
XX
DE Human; serum albumin; biopolymer marker; SELDI;
KW Surface Enhanced Laser Desorption Ionization mass spectrometry;
KW time-of-flight detection procedure; complement system disease;
KW syndrome X; insulin resistance; hyperinsulinaemia.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "Optionally absent"
FT FT
FT Misc-difference 2. .25 /note= "Specifically claimed in claim 1"
FT FT
FT Misc-difference 26 /note= "Optionally absent"
FT FT
XX US2002160531-A1.
XX
XX 31-OCT-2002.
XX
XX 30-APR-2001; 2001US-00846328.
XX
XX 30-APR-2001; 2001US-00846328.
XX
XX (JACK/) JACKOWSKI G.
PA (THAT/) THATCHER B.
PA (MARS/) MARSHALL J.
PA (YANT/) YANTHA J.
PA (VREE/) VREES T.
XX
PI Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;
XX
XX WPI; 2003-255195/25.
XX
XX A new biopolymer marker useful in indicating a particular disease state
XX particularly insulin resistance.
XX
XX Disclosure; Fig 1; 10pp; English.

CC The invention describes a biopolymer marker useful in indicating at least
CC one particular disease state. Biopolymer markers are identified using
CC Surface Enhanced Laser Desorption Ionization (SELDI) mass spectrometry
CC and time-of-flight detection procedures. The markers are useful for
CC indicating e.g. complement system diseases and syndrome X, characterised
CC by the clustering of insulin resistance and hyperinsulinaemia. This is
CC the amino acid sequence of a human serum albumin biopolymer marker useful
CC for indicating insulin resistance
XX
SQ Sequence 26 AA;

Query Match 100.0%; Score 123; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 1.6e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFKDLGEENFKALVL 24
DB 2 DAHKSEVAHRFKDLGEENFKALVL 25
|||||

RESULT 3
ABU08847
ID ABU08847 standard; peptide; 28 AA.
XX
AC ABU08847;
XX
DT 25-AUG-2003 (first entry)
XX
DE Serum albumin peptide, #4, used for physiological condition diagnostics.
XX
DE Proteomic; human; physiological condition; analyte; biopolymer;
KW Biomarker; serum albumin; insulin resistance.
XX
OS Homo sapiens.
XX
PN US2002160420-A1.
XX
PD 31-OCT-2002.
XX
PF 30-APR-2001; 2001US-00846330.
XX
PR 30-APR-2001; 2001US-00846330.
XX
PA (JACK/) JACKOWSKI G.
PA (THAT/) THATCHER B.
PA (MARS/) MARSHALL J.
PA (YANT/) YANTHA J.
PA (VREE/) VREES T.
XX
PI Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;
XX
XX WPI; 2003-491923/46.
XX
XX Determining proteomic basis e.g. basis for diagnosing existence of or
PT predicting development and/or progression of abnormal physiological
PT conditions based upon the presence of proteomic materials.
XX
XX Disclosure; Page 22; 25pp; English.

CC The invention discloses a method for determining a proteomic basis for
CC development and progression of abnormal physiological conditions. The
CC method comprises isolating one or more patient specific proteomic
CC materials from a sample and comparing it against a library of proteomic
CC materials having characteristics identifiable with both normal and
CC abnormal physiological conditions or their predictive hallmarks. The
CC method is useful for determining a proteomic basis for development and
CC progression of abnormal physiological conditions. The method is also
CC useful for evaluating samples containing several analytes/biopolymers for
CC the presence of physiological condition specific sequences. The peptide
CC presented is a biomarker from serum albumin and is associated with
CC insulin resistance
XX
SQ Sequence 28 AA;

Query Match 100.0%; Score 123; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.7e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFKDLGEENFKALVL 24
DB 2 DAHKSEVAHRFKDLGEENFKALVL 25
|||||


```

KW nervous system disorders; arthritis; inflammation.
XX Homo sapiens.
XX WO200164835-A2.
XX 07-SEP-2001.
XX
XX 26-FEB-2001; 2001WO-US004927.
XX
XX 28-FEB-2000; 2000US-00515126.
XX 18-MAY-2000; 2000US-00577409.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-514838/56.
XX N-PSDB; AA191563.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
XX and treating e.g. leukemia, inflammation and immune disorders.
XX
XX Claim 20; SEQ ID NO 25524; 1399pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AA179941-AA193841) and
XX the encoded proteins (AA000010-AA03910) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 119 AA;
XX
XX Query Match 100.0%; Score 123; DB 4; Length 119;
XX Best Local Similarity 100.0%; Pred. No. 8.8e-12;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGEENFKALVL 24
Db 30 DAHKSEVAHRFKDLGEENFKALVL 53

RESULT 7
AAP30004
ID AAP30004 standard; protein; 133 AA.
XX
XX AAP30004;
XX
XX 25-APR-1992 (first entry)
XX
XX Sequence encoded by recombinant DNA molecule pKT218(HSA/33-1 (BgIII-
XX EcoRI)-HSA/17-3 (BgIII-EcoRI)) human proserum albumin.
XX
XX Burn therapy; blood; protein; nitrogen fixation; food additive;
XX kernicterus therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..26
XX /label= signal
XX Protein 27..59
XX /label= residues 1-33
XX Protein 60..92
XX /label= residues 319-351
XX

nervous system disorders; arthritis; inflammation.
Homo sapiens.
WO200164835-A2.
07-SEP-2001.
26-FEB-2001; 2001WO-US004927.
28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
(HYSE-) HYSEQ INC.
Tang YT, Liu C, Drmanac RT;
WPI; 2001-514838/56.
N-PSDB; AA191563.
Isolated nucleic acids and polypeptides, useful for preventing diagnosing
and treating e.g. leukemia, inflammation and immune disorders.
Claim 20; SEQ ID NO 25524; 1399pp + Sequence Listing; English.
The invention relates to human polynucleotides (AA179941-AA193841) and
the encoded proteins (AA000010-AA03910) that exhibit activity elating to
cytokine, cell proliferation or cell differentiation or which may induce
production of other cytokines in other cell populations. The
polynucleotides and polypeptides are useful in gene therapy, vaccines or
peptide therapy. The polypeptides have various cytokine-like activities,
e.g. stem cell growth factor activity, haematopoiesis regulating
activity, tissue growth factor activity, immunomodulatory activity and
activin/inhibin activity and may be useful in the diagnosis and/or
treatment of cancer, leukaemia, nervous system disorders, arthritis and
inflammation. Note: The sequence data for this patent did not form part
of the printed specification, but was obtained in electronic format
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 119 AA;

Query Match 100.0%; Score 123; DB 4; Length 119;
Best Local Similarity 100.0%; Pred. No. 8.8e-12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGEENFKALVL 24
Db 30 DAHKSEVAHRFKDLGEENFKALVL 53

RESULT 7
AAP30004
ID AAP30004 standard; protein; 133 AA.
XX
XX AAP30004;
XX
XX 25-APR-1992 (first entry)
XX
XX Sequence encoded by recombinant DNA molecule pKT218(HSA/33-1 (BgIII-
XX EcoRI)-HSA/17-3 (BgIII-EcoRI)) human proserum albumin.
XX
XX Burn therapy; blood; protein; nitrogen fixation; food additive;
XX kernicterus therapy.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 1..26
XX /label= signal
XX Protein 27..59
XX /label= residues 1-33
XX Protein 60..92
XX /label= residues 319-351
XX

Protein 93..124
/label= residues 368-399
Protein 125..133
/label= residues 572-580
EP91527-A.
19-OCT-1983.
14-DEC-1981; 81US-00330912.
14-DEC-1981; 81US-00330912.
(HARD ) HARVARD COLLEGE.
Gilbert W, Philipp BW;
WPI; 1983-796520/43.
N-PSDB; AAN30009.
Prodn. of human serum albumin-like polypeptide(s) - from host transformed
with recombinant DNA molecule.
Example; Fig 4; 42pp; English.
AAN30009 was prepd. from two clones isolated from a human fetal liver
cDNA library screened with mouse serum albumin cDNA. The two clones are
pKT218(HSA/33-1) and pKT218(HSA/17-3), which were recombined to give
AAN30009, the coding sequence of which is out of phase by a single
nucleotide (see FT). However, as a result of perhaps some internal
start, hosts transformed with the hybrid gene (even out of phase) in
pKT218 still produce HSA-like products
Sequence 133 AA;

Query Match 100.0%; Score 123; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 1e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGEENFKALVL 24
Db 27 DAHKSEVAHRFKDLGEENFKALVL 50

RESULT 8
AAU29875
ID AAU29875 standard; protein; 192 AA.
XX
XX AAU29875;
XX
XX 18-DEC-2001 (first entry)
XX
XX Novel human secreted protein #366.
XX
XX Human; vaccination; gene therapy; nutritional supplement;
XX stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
XX Homo sapiens.
XX
XX WO200179449-A2.
XX
XX 25-OCT-2001.
XX
XX 16-APR-2001; 2001WO-US008656.
XX
XX 18-APR-2000; 2000US-00552929.
XX 26-JAN-2001; 2001US-00770160.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX

```

DR WPI; 2001-611725/70.
 XX Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy.
 PT
 XX
 PS
 PS
 XX
 XX
 CC Claim 20; Page 206; 765pp; English.
 CC
 CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising the
 CC nucleic acids encoding the polypeptides and cells genetically engineered
 CC to express them are also useful for producing the proteins. The proteins
 CC are useful in genetic vaccination, testing and therapy, and can be used
 CC as nutritional supplements. They may be used to increase stem cell
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
 CC and/or nerve tissue growth or regeneration; immune suppression and/or
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
 CC AAU29510-AAU3304 represent the amino acid sequences of novel human
 CC secreted proteins of the invention
 XX
 XX
 SQ Sequence 192 AA;
 Query Match 100.0%; Score 123; DB 4; Length 192;
 Best Local Similarity 100.0%; Pred. No. 1.5e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAHKSEVAHRFKDLGEENFKALVL 24
 DB 53 DAHKSEVAHRFKDLGEENFKALVL 76
 RESULT 9
 AA017048
 ID AA017048 standard; protein; 195 AA.
 XX
 AC AA017048;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Human serum albumin (1-195) SEQ ID NO: 56.
 XX
 XX Alpha-MSH; inflammation; autoimmune disease; gene therapy; sepsis;
 KW alpha-melanocyte stimulating hormone; rheumatoid arthritis; asthma;
 KW cirrhosis; dermatitis; psoriasis; inflammatory bowel disease;
 KW immunosuppressive; antiinflammatory; antirheumatic; antiarthritic;
 KW antiasthmatic; antibacterial; dermatological; antipsoriatic;
 KW antidiabetic; ophthalmological; neuroprotective; multiple sclerosis;
 KW diabetes; uveitis; coeliac disease.
 XX
 XX Homo sapiens.
 OS
 XX WO200206316-A2.
 FN
 XX 24-JAN-2002.
 PD
 XX 16-JUN-2001; 2001WO-US022263.
 PF
 XX 14-JUL-2000; 2000US-0218381P.
 PR 18-AUG-2000; 2000US-0226382P.
 PR 06-OCT-2000; 2000US-0238380P.
 PR 29-DEC-2000; 2000US-0258764P.
 PR 14-JUN-2001; 2001US-0298317P.
 XX
 XX (ZYCO-) ZYCO INC.
 FA
 XX Hedley ML, Urban R, Aziz N, Chen H, Etemad-Moghadam B, Yin P;
 PI
 XX WPI; 2002-195801/25.
 DR

XX Novel nucleic acid encoding fusion protein comprising alpha-melanocyte
 PT stimulating hormone concatamer or its analog, for treating inflammatory
 PT or autoimmune disorders.
 XX
 PS
 PS
 XX
 XX
 CC Example 2; Page 46; 89pp; English.
 CC
 CC The present invention relates to a nucleic acid comprising a sequence
 CC encoding a fusion polypeptide having an alpha-melanocyte stimulating
 CC hormone (MSH) concatamer. The sequences are useful for treating an
 CC individual suffering from, or at risk of, a disorder of the immune system
 CC e.g. inflammatory disorder or autoimmune disorder, including rheumatoid
 CC arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact
 CC hypersensitivity, inflammatory bowel disease, autoimmune encephalitis,
 CC multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The
 CC present sequence is a protein described in the exemplification of the
 CC invention
 XX
 XX
 SQ Sequence 195 AA;
 Query Match 100.0%; Score 123; DB 5; Length 195;
 Best Local Similarity 100.0%; Pred. No. 1.6e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAHKSEVAHRFKDLGEENFKALVL 24
 DB 1 DAHKSEVAHRFKDLGEENFKALVL 24
 RESULT 10
 ABU10022
 ID ABU10022 standard; protein; 195 AA.
 XX
 AC ABU10022;
 XX
 DT 31-JUL-2003 (first entry)
 XX
 DE Human serum albumin residues 1-195.
 XX
 KW Bladder disorder; cytostatic; antiinflammatory; immune response;
 KW un-methylated CpG sequence; alpha-MSH; melanocortin receptor;
 KW bladder cancer; tumour; interstitial cystitis; inflammation;
 KW alpha-MSH concatamer; melanocyte stimulating hormone; human;
 KW serum albumin.
 XX
 XX Homo sapiens.
 OS
 XX US2002193332-A1.
 PN
 XX 19-DEC-2002.
 PD
 XX 12-FEB-2002; 2002US-00074956.
 PF
 XX 12-FEB-2001; 2001US-0268175P.
 PR
 XX (HEDL/) HEDLEY M L.
 PA
 XX Hedley ML;
 FI
 XX WPI; 2003-447327/42.
 DR
 XX
 XX Modulating immune responses in a mammal with a bladder disorder e.g.
 PT bladder cancer, by administering nucleic acids comprising un-methylated
 PT CpG sequences, nucleic acids encoding alpha-MSH, or alpha-MSH peptides to
 PT the mammal.
 XX
 XX Example 2; Page 9; 17pp; English.
 PS
 XX The invention describes a method of modulating an immune response in a
 CC mammal, comprising identifying a mammal that has or is at risk for having
 CC a bladder disorder, and administering: (a) an isolated nucleic acid (N1)
 CC comprising an un-methylated CpG sequence to the mammal; (b) an isolated
 CC nucleic acid (N2) comprising sequence encoding alpha-MSH to the mammal;

CC or (c) a peptide that binds to a melanocortin receptor to the mammal. The
 CC method is useful for modulating immune response in a mammal having a
 CC bladder disorder, where administration of (N1) results in an amelioration
 CC of one or more symptoms of the disorder. Preferably, the method is useful
 CC for modulating immune response in a mammal having bladder cancer (where
 CC administration of (N1) results in a decrease in tumour size or activity),
 CC or for modulating immune response in a mammal having interstitial
 CC cystitis (where administration of (N1) results in a modulation of the
 CC immune response from Th2 response to a Th1 response). The method is also
 CC useful for modulating immune response in a mammal having bladder disorder
 CC that is characterised by inflammation which is associated with symptoms
 CC of interstitial cystitis or associated with a disruption of the integrity
 CC of the bladder lining. This is the amino acid sequence of human serum
 CC albumin residues 1-195 that can be used in the creation of melanocyte
 CC stimulating hormone (alpha-MSH) concatamers resulting in secretion of the
 CC fusion protein when expressed in mammalian cells
 XX
 SQ Sequence 195 AA;

Query Match 100.0%; Score 123; DB 7; Length 195;
 Best Local Similarity 100.0%; Pred. No. 1.6e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAKSEVAHRFKDLGSENFKALVL 24
 |||||
 DB 1 DAKSEVAHRFKDLGSENFKALVL 24

RESULT 11
 AAY83947
 ID AAY83947 standard; protein; 204 AA.
 XX
 AC AAY83947;

DT 28-JUL-2000 (first entry)

DE Yeast codon-biased recombinant HSA protein fragment HSA-I.

XX Recombinant; human serum albumin; HSA; yeast codon bias; host cell;
 KW overlapping oligonucleotide; expression vector.

XX Homo sapiens.
 OS Synthetic.

XX CN1239103-A.

XX 22-DEC-1999.

XX 17-JUN-1998; 98CN-00102506.

XX 17-JUN-1998; 98CN-00102506.

XX (HAIJ-) HAIJI BIOENGINEERING CO LTD.

XX Li S, Lu D;

XX WPI; 2000-351198/31.
 DR N-PSDB; AAA10092.

XX Process for preparing recombinant human serum albumin comprising yeast
 PT biased sex codons - uses a recombinant DNA technique.

XX Example 1; Fig 3; 44pp; Chinese.

XX The method relates to a method of recombinantly producing human serum
 CC albumin (HSA) in yeast by altering the coding sequence of HSA to comprise
 CC a yeast codon bias. The complete HSA gene (AAA10091) was generated as
 CC three synthetic fragments (AAA10092-AAA10094) joined by recombinant DNA
 CC technology. Each HSA fragment was synthesised from overlapping
 CC oligonucleotide fragments that were extended. This sequence represents
 CC the sequence of the HSA fragment HSA-I encoded by the human gene with a
 CC yeast codon bias. The invention also covers a recombinant expression
 CC vector, yeast host cells carrying the recombinant expression vector and

CC the process for producing human serum albumin in the yeast host cell,
 CC especially in secretory mode
 XX
 SQ Sequence 204 AA;

Query Match 100.0%; Score 123; DB 3; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1.6e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAKSEVAHRFKDLGSENFKALVL 24
 |||||
 DB 8 DAKSEVAHRFKDLGSENFKALVL 31

RESULT 12
 AAU29874
 ID AAU29874 standard; protein; 214 AA.

XX
 AC AAU29874;

XX 18-DEC-2001 (first entry)

XX Novel human secreted protein #365.

XX Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX Homo sapiens.

XX WO200179449-A2.

XX 25-OCT-2001.

XX 16-APR-2001; 2001WO-US008656.

XX 18-APR-2000; 2000US-00552929.

XX 26-JAN-2001; 2001US-00770160.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI; 2001-611725/70.

XX Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy.

XX Claim 20; Page 205; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising the
 CC nucleic acids encoding the polypeptides and cells genetically engineered
 CC to express them are also useful for producing the proteins. The proteins
 CC are useful in genetic vaccination, testing and therapy, and can be used
 CC as nutritional supplements. They may be used to increase stem cell
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
 CC and/or nerve tissue growth or regeneration; immune suppression and/or
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
 CC AAU29510-AAU33304 represent the amino acid sequences of novel human
 CC secreted proteins of the invention

XX Sequence 214 AA;

Query Match 100.0%; Score 123; DB 4; Length 214;
 Best Local Similarity 100.0%; Pred. No. 1.7e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGEENFKALVL 24
 Db 37 DAHKSEVAHRFKDLGEENFKALVL 60

RESULT 13
 AAO17051
 ID AAO17051 standard; protein; 236 AA.
 AC AAO17051;
 XX
 XX 29-MAY-2002 (first entry)
 DT Human albumin-thrombin-alpha-MSH SEQ ID NO: 82.
 DE
 XX Alpha-MSH; inflammation; autoimmune disease; gene therapy; sepsis;
 KW alpha-melanocyte stimulating hormone; rheumatoid arthritis; asthma;
 KW cirrhosis; dermatitis; psoriasis; inflammatory bowel disease;
 KW immunosuppressive; antinflammatory; antirheumatic; antiarthritic;
 KW antiaesthetic; antibacterial; dermatological; antipsoriatic;
 KW antidiabetic; ophthalmological; neuroprotective; multiple sclerosis;
 KW diabetes; uveitis; coeliac disease.
 XX Homo sapiens.
 OS
 XX WO200206316-A2.
 PN
 XX 24-JAN-2002.
 PD
 XX 16-JUL-2001; 2001WO-US022263.
 PF
 XX 14-JUL-2000; 2000US-0218381P.
 PR 18-AUG-2000; 2000US-0226382P.
 PR 06-OCT-2000; 2000US-0238380P.
 PR 29-DEC-2000; 2000US-0258764P.
 PR 14-JUN-2001; 2001US-0298317P.
 XX (ZYCO-) ZYCOS INC.
 PA
 XX Hedley ML, Urban R, Aziz N, Chen H, Etemad-Moghadam B, Yin P;
 PI WPI; 2002-195801/25.
 XX Novel nucleic acid encoding fusion protein comprising alpha-melanocyte
 DR stimulating hormone concatamer or its analog, for treating inflammatory
 XX or autoimmune disorders.
 XX Example 2; Page 48; 89pp; English.
 PS The present invention relates to a nucleic acid comprising a sequence
 XX encoding a fusion polypeptide having an alpha-melanocyte stimulating
 CC hormone (MSH) concatamer. The sequences are useful for treating an
 CC individual suffering from, or at risk of, a disorder of the immune system
 CC e.g. inflammatory disorder or autoimmune disorder, including rheumatoid
 CC arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact
 CC hypersensitivity, inflammatory bowel disease, autoimmune encephalitis,
 CC multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The
 CC present sequence is a peptide described in the exemplification of the
 CC invention
 XX Sequence 236 AA;
 SQ Query Match 100.0%; Score 123; DB 5; Length 236;
 Best Local Similarity 100.0%; Pred. No. 1.9e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGEENFKALVL 24
 Db 25 DAHKSEVAHRFKDLGEENFKALVL 48

RESULT 14
 AAO16984
 ID AAO16984 standard; protein; 241 AA.
 AC AAO16984;
 XX
 XX 29-MAY-2002 (first entry)
 DT Alpha-MSH construct protein fragment SEQ ID NO: 59.
 DE
 XX Alpha-MSH; inflammation; autoimmune disease; gene therapy; sepsis;
 KW alpha-melanocyte stimulating hormone; rheumatoid arthritis; asthma;
 KW cirrhosis; dermatitis; psoriasis; inflammatory bowel disease;
 KW immunosuppressive; antinflammatory; antirheumatic; antiarthritic;
 KW antiaesthetic; antibacterial; dermatological; antipsoriatic;
 KW antidiabetic; ophthalmological; neuroprotective; multiple sclerosis;
 KW diabetes; uveitis; coeliac disease.
 XX Unidentified.
 OS
 XX WO200206316-A2.
 PN
 XX 24-JAN-2002.
 PD
 XX 16-JUL-2001; 2001WO-US022263.
 PF
 XX 14-JUL-2000; 2000US-0218381P.
 PR 18-AUG-2000; 2000US-0226382P.
 PR 06-OCT-2000; 2000US-0238380P.
 PR 29-DEC-2000; 2000US-0258764P.
 PR 14-JUN-2001; 2001US-0298317P.
 XX (ZYCO-) ZYCOS INC.
 PA
 XX Hedley ML, Urban R, Aziz N, Chen H, Etemad-Moghadam B, Yin P;
 PI WPI; 2002-195801/25.
 XX Novel nucleic acid encoding fusion protein comprising alpha-melanocyte
 DR stimulating hormone concatamer or its analog, for treating inflammatory
 XX or autoimmune disorders.
 XX Example 2; Page 4-5; 89pp; English.
 PS The present invention relates to a nucleic acid comprising a sequence
 XX encoding a fusion polypeptide having an alpha-melanocyte stimulating
 CC hormone (MSH) concatamer. The sequences are useful for treating an
 CC individual suffering from, or at risk of, a disorder of the immune system
 CC e.g. inflammatory disorder or autoimmune disorder, including rheumatoid
 CC arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact
 CC hypersensitivity, inflammatory bowel disease, autoimmune encephalitis,
 CC multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The
 CC present sequence is a protein described in the exemplification of the
 CC invention
 XX Sequence 241 AA;
 SQ Query Match 100.0%; Score 123; DB 5; Length 241;
 Best Local Similarity 100.0%; Pred. No. 2e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGEENFKALVL 24
 Db 25 DAHKSEVAHRFKDLGEENFKALVL 48

RESULT 15
 ABU10025
 ID ABU10025 standard; protein; 241 AA.
 AC ABU10025;
 XX
 XX 31-JUL-2003 (first entry)
 DT
 XX

KW diabetes; uveitis; coeliac disease.
 XX
 OS Unidentified.
 XX
 PN WO200206316-A2.
 XX
 XX 24-JAN-2002.
 PD
 XX 16-JUL-2001; 2001WO-US022263.
 PF
 XX 14-JUL-2000; 2000US-0218381P.
 PR 18-AUG-2000; 2000US-0226382P.
 PR 06-OCT-2000; 2000US-0238380P.
 PR 29-DEC-2000; 2000US-0258764P.
 PR 14-JUN-2001; 2001US-0298317P.
 XX
 XX (ZYCO-) ZYCOS INC.
 PA
 XX Hedley ML, Urban R, Aziz N, Chen H, Etemad-Moghadam B, Yin P;
 PI WPI; 2002-195801/25.
 XX
 DR Novel nucleic acid encoding fusion protein comprising alpha-melanocyte
 XX stimulating hormone concatamer or its analog, for treating inflammatory
 XX or autoimmune disorders.
 XX
 PS Disclosure; Page 5; 89pp; English.
 XX
 XX The present invention relates to a nucleic acid comprising a sequence
 CC encoding a fusion polypeptide having an alpha-melanocyte stimulating
 CC hormone (MSH) concatamer. The sequences are useful for treating an
 CC individual suffering from, or at risk of, a disorder of the immune system
 CC e.g. inflammatory disorder or autoimmune disorder, including rheumatoid
 CC arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact
 CC hypersensitivity, inflammatory bowel disease, autoimmune encephalitis,
 CC multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The
 CC present sequence is a protein described in the exemplification of the
 CC invention.
 XX
 SQ Sequence 244 AA;
 XX
 Query Match 100.0%; Score 123; DB 5; Length 244;
 Best Local Similarity 100.0%; Pred. No. 2e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAHSEVAHRFKDLGEENFKALVL 24
 DB 25 DAHSEVAHRFKDLGEENFKALVL 48
 XX
 RESULT 18
 AAO16987
 ID AAO16987 standard; protein; 245 AA.
 AC AAO16987;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Alpha-MSH construct protein fragment SEQ ID NO: 72.
 XX
 KW Alpha-MSH; inflammation; autoimmune disease; gene therapy; sepsis;
 KW alpha-melanocyte stimulating hormone; rheumatoid arthritis; asthma;
 KW cirrhosis; dermatitis; psoriasis; inflammatory bowel disease;
 KW immunosuppressive; antiinflammatory; antirheumatic; antiarthritic;
 KW antiasthmatic; antibacterial; dermatological; antipsoriatic;
 KW antidiabetic; ophthalmological; neuroprotective; multiple sclerosis;
 KW diabetes; uveitis; coeliac disease.
 XX
 OS Unidentified.
 XX
 PN WO200206316-A2.
 XX
 XX 24-JAN-2002.
 PD

XX 16-JUL-2001; 2001WO-US022263.
 PF
 XX 14-JUL-2000; 2000US-0218381P.
 PR 18-AUG-2000; 2000US-0226382P.
 PR 06-OCT-2000; 2000US-0238380P.
 PR 29-DEC-2000; 2000US-0258764P.
 PR 14-JUN-2001; 2001US-0298317P.
 XX
 XX (ZYCO-) ZYCOS INC.
 PA
 XX Hedley ML, Urban R, Aziz N, Chen H, Etemad-Moghadam B, Yin P;
 PI WPI; 2002-195801/25.
 XX
 DR Novel nucleic acid encoding fusion protein comprising alpha-melanocyte
 XX stimulating hormone concatamer or its analog, for treating inflammatory
 XX or autoimmune disorders.
 XX
 PS Disclosure; Page 5; 89pp; English.
 XX
 XX The present invention relates to a nucleic acid comprising a sequence
 CC encoding a fusion polypeptide having an alpha-melanocyte stimulating
 CC hormone (MSH) concatamer. The sequences are useful for treating an
 CC individual suffering from, or at risk of, a disorder of the immune system
 CC e.g. inflammatory disorder or autoimmune disorder, including rheumatoid
 CC arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact
 CC hypersensitivity, inflammatory bowel disease, autoimmune encephalitis,
 CC multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The
 CC present sequence is a protein described in the exemplification of the
 CC invention.
 XX
 SQ Sequence 245 AA;
 XX
 Query Match 100.0%; Score 123; DB 5; Length 245;
 Best Local Similarity 100.0%; Pred. No. 2e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DAHSEVAHRFKDLGEENFKALVL 24
 DB 25 DAHSEVAHRFKDLGEENFKALVL 48
 XX
 RESULT 19
 AAO16988
 ID AAO16988 standard; protein; 245 AA.
 AC AAO16988;
 XX
 DT 29-MAY-2002 (first entry)
 XX
 DE Alpha-MSH construct protein fragment SEQ ID NO: 73.
 XX
 KW Alpha-MSH; inflammation; autoimmune disease; gene therapy; sepsis;
 KW alpha-melanocyte stimulating hormone; rheumatoid arthritis; asthma;
 KW cirrhosis; dermatitis; psoriasis; inflammatory bowel disease;
 KW immunosuppressive; antiinflammatory; antirheumatic; antiarthritic;
 KW antiasthmatic; antibacterial; dermatological; antipsoriatic;
 KW antidiabetic; ophthalmological; neuroprotective; multiple sclerosis;
 KW diabetes; uveitis; coeliac disease.
 XX
 OS Unidentified.
 XX
 PN WO200206316-A2.
 XX
 XX 24-JAN-2002.
 PD

XX 16-JUL-2001; 2001WO-US022263.
 PF
 XX 14-JUL-2000; 2000US-0218381P.
 PR 18-AUG-2000; 2000US-0226382P.
 PR 06-OCT-2000; 2000US-0238380P.
 PR 29-DEC-2000; 2000US-0258764P.
 XX

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PR 14-JUN-2001; 2001US-0298317P.
XX
XX PA (ZYCO-) ZYCOS INC.
XX
XX PI Hedley ML, Urban R, Aziz N, Chen H, Etemad-Moghadam B, Yin P;
XX
XX DR WPI; 2002-195801/25.
XX
XX PT Novel nucleic acid encoding fusion protein comprising alpha-melanocyte
XX PT stimulating hormone concatamer or its analog, for treating inflammatory
XX PT or autoimmune disorders.
XX
XX PS Disclosure; Page 5; 89pp; English.
XX
XX CC The present invention relates to a nucleic acid comprising a sequence
XX CC encoding a fusion polypeptide having an alpha-melanocyte stimulating
XX CC hormone (MSH) concatamer. The sequences are useful for treating an
XX CC individual suffering from, or at risk of, a disorder of the immune system
XX CC e.g. inflammatory disorder or autoimmune disorder, including rheumatoid
XX CC arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact
XX CC hypersensitivity, inflammatory bowel disease, autoimmune encephalitis,
XX CC multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The
XX CC present sequence is a protein described in the exemplification of the
XX CC invention
XX
XX SQ Sequence 245 AA;
Query Match 100.0%; Score 123; DB 5; Length 245;
Best Local Similarity 100.0%; Pred. No. 2e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGEENFKALVL 24
Db 25 DAHKSEVAHRFKDLGEENFKALVL 48

RESULT 20
AA016989
ID AAO16989 standard; protein; 268 AA.
XX
XX AC AAO16989;
XX
XX DT 29-MAY-2002 (first entry)
XX
XX DE Alpha-MSH construct protein fragment SEQ ID NO: 60.
XX
XX KW Alpha-MSH; inflammation; autoimmune disease; gene therapy; sepsis;
XX KW alpha-melanocyte stimulating hormone; rheumatoid arthritis; asthma;
XX KW cirrhosis; dermatitis; psoriasis; inflammatory bowel disease;
XX KW immunosuppressive; antiinflammatory; antirheumatic; antiarthritic;
XX KW antiasthmatic; antibacterial; dermatological; antipsoriatic;
XX KW antidiabetic; ophthalmological; neuroprotective; multiple sclerosis;
XX KW diabetes; uveitis; coeliac disease.
XX
XX OS Unidentified.
XX
XX PN WO200206316-A2.
XX
XX PD 24-JAN-2002.
XX
XX PF 16-JUL-2001; 2001WO-US022263.
XX
XX PR 14-JUL-2000; 2000US-0218381P.
XX PR 18-AUG-2000; 2000US-0226382P.
XX PR 06-OCT-2000; 2000US-0238380P.
XX PR 29-DEC-2000; 2000US-0258764P.
XX PR 14-JUN-2001; 2001US-0298317P.
XX
XX PA (ZYCO-) ZYCOS INC.
XX
XX PI Hedley ML, Urban R, Aziz N, Chen H, Etemad-Moghadam B, Yin P;
XX
XX DR WPI; 2002-195801/25.
XX
XX PT Novel nucleic acid encoding fusion protein comprising alpha-melanocyte
XX PT stimulating hormone concatamer or its analog, for treating inflammatory
XX PT or autoimmune disorders.
XX
XX PS Example 2; Page 5; 89pp; English.
XX
XX CC The present invention relates to a nucleic acid comprising a sequence
XX CC encoding a fusion polypeptide having an alpha-melanocyte stimulating
XX CC hormone (MSH) concatamer. The sequences are useful for treating an
XX CC individual suffering from, or at risk of, a disorder of the immune system
XX CC e.g. inflammatory disorder or autoimmune disorder, including rheumatoid
XX CC arthritis, asthma, sepsis, cirrhosis, dermatitis, psoriasis, contact
XX CC hypersensitivity, inflammatory bowel disease, autoimmune encephalitis,
XX CC multiple sclerosis, diabetes, lupus, uveitis and coeliac disease. The
XX CC present sequence is a protein described in the exemplification of the
XX CC invention
XX
XX SQ Sequence 268 AA;
Query Match 100.0%; Score 123; DB 5; Length 268;
Best Local Similarity 100.0%; Pred. No. 2.2e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGEENFKALVL 24
Db 25 DAHKSEVAHRFKDLGEENFKALVL 48

RESULT 21
ABU10026
ID ABU10026 standard; protein; 268 AA.
XX
XX AC ABU10026;
XX
XX DT 31-JUL-2003 (first entry)
XX
XX DE Alpha-MSH/Serum albumin fusion protein H4.
XX
XX KW Bladder disorder; cytostatic; antiinflammatory; immune response;
XX KW un-methylated CpG sequence; alpha-MSH; melanocortin receptor;
XX KW bladder cancer; tumour; interstitial cystitis; inflammation;
XX KW alpha-MSH concatamer; melanocyte stimulating hormone; human;
XX KW serum albumin; fusion protein; H4.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX PN US2002193332-A1.
XX
XX PD 19-DEC-2002.
XX
XX PF 12-FEB-2002; 2002US-00074956.
XX
XX PR 12-FEB-2001; 2001US-0268175P.
XX
XX PA (HEDL/) HEDLEY M L.
XX
XX PI Hedley ML;
XX
XX DR WPI; 2003-447327/42.
XX
XX PT Modulating immune responses in a mammal with a bladder disorder e.g.
XX PT bladder cancer, by administering nucleic acids comprising un-methylated
XX PT CpG sequences, nucleic acids encoding alpha-MSH, or alpha-MSH peptides to
XX PT the mammal.
XX
XX PS Example 2; Page 9; 17pp; English.
XX
XX CC The invention describes a method of modulating an immune response in a
XX CC mammal, comprising identifying a mammal that has or is at risk for having
XX CC a bladder disorder, and administering: (a) an isolated nucleic acid (NI)
XX CC comprising an un-methylated CpG sequence to the mammal; (b) an isolated

```

CC nucleic acid (N2) comprising sequence encoding alpha-MSH to the mammal;
 CC or (c) a peptide that binds to a melanocortin receptor to the mammal. The
 CC method is useful for modulating immune response in a mammal having a
 CC bladder disorder, where administration of (N1) results in an amelioration
 CC of one or more symptoms of the disorder. Preferably, the method is useful
 CC for modulating immune response in a mammal having bladder cancer (where
 CC administration of (N1) results in a decrease in tumour size or activity),
 CC or for modulating immune response in a mammal having interstitial
 CC cystitis (where administration of (N1) results in a modulation of the
 CC immune response from Th2 response to a Th1 response). The method is also
 CC useful for modulating immune response in a mammal having bladder disorder
 CC that is characterised by inflammation which is associated with symptoms
 CC of interstitial cystitis or associated with a disruption of the integrity
 CC of the bladder lining. This is the amino acid sequence of a human serum
 CC melanocyte stimulating hormone (alpha-MSH) concatamer useful in the
 CC treatment of bladder disorders
 XX
 SQ Sequence 268 AA;

Query Match 100.0%; Score 123; DB 7; Length 268;
 Best Local Similarity 100.0%; Pred. No. 2.2e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFKDLGEENFKALVL 24
 DB 25 DAHKSEVAHRFKDLGEENFKALVL 48
 |||||

RESULT 22
 AAU29581
 ID AAU29581 standard; protein; 289 AA.
 AC AAU29581;
 XX
 XX 18-DEC-2001 (first entry)
 XX
 XX Novel human secreted protein #72.
 XX Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX Homo sapiens.
 OS
 XX WO200179449-A2.
 XX
 XX 25-OCT-2001.
 XX 16-APR-2001; 2001WO-US008656.
 XX 18-APR-2000; 2000US-00552929.
 PR 26-JAN-2001; 2001US-00770160.
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Drmanac RT;
 PI WPI; 2001-611725/70.
 XX Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy.
 XX Claim 20; Page 168; 765pp; English.

CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising the
 CC nucleic acids encoding the polypeptides and cells genetically engineered

CC to express them are also useful for producing the proteins. The proteins
 CC are useful in genetic vaccination, testing and therapy, and can be used
 CC as nutritional supplements. They may be used to increase stem cell
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
 CC and/or nerve tissue growth or regeneration; immune suppression and/or
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
 CC AAU29510-AAU33304 represent the amino acid sequences of novel human
 CC secreted proteins of the invention
 XX
 SQ Sequence 289 AA;

Query Match 100.0%; Score 123; DB 4; Length 289;
 Best Local Similarity 100.0%; Pred. No. 2.4e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFKDLGEENFKALVL 24
 DB 37 DAHKSEVAHRFKDLGEENFKALVL 60
 |||||

RESULT 23
 AAU29575
 ID AAU29575 standard; protein; 289 AA.
 AC AAU29575;
 XX
 XX 18-DEC-2001 (first entry)
 XX
 XX Novel human secreted protein #66.

XX Human; vaccination; gene therapy; nutritional supplement;
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
 XX Homo sapiens.
 OS
 XX WO200179449-A2.
 XX
 XX 25-OCT-2001.
 XX 16-APR-2001; 2001WO-US008656.
 XX 18-APR-2000; 2000US-00552929.
 PR 26-JAN-2001; 2001US-00770160.
 XX (HYSE-) HYSEQ INC.
 PA
 XX Tang YT, Liu C, Drmanac RT;
 PI WPI; 2001-611725/70.
 XX Nucleic acids encoding a range of human polypeptides, useful in genetic
 PT vaccination, testing and therapy.
 XX Claim 20; Page 167; 765pp; English.

CC The invention relates to novel human secreted polypeptides. The
 CC polypeptides and antibodies to the polypeptides are useful for
 CC determining the presence of or predisposition to a disease associated
 CC with altered levels of polypeptide. The polypeptides are also useful for
 CC identifying agents (agonists and antagonists) that bind to them. Cells
 CC expressing the proteins are useful for identifying a therapeutic agent
 CC for use in treatment of a pathology related to aberrant expression or
 CC physiological interactions of the polypeptide. Vectors comprising the
 CC nucleic acids encoding the polypeptides and cells genetically engineered
 CC to express them are also useful for producing the proteins. The proteins
 CC are useful in genetic vaccination, testing and therapy, and can be used
 CC as nutritional supplements. They may be used to increase stem cell
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
 CC and/or nerve tissue growth or regeneration; immune suppression and/or
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
 CC AAU29510-AAU33304 represent the amino acid sequences of novel human
 CC secreted proteins of the invention

```
XX SQ Sequence 289 AA;
Query Match 100.0%; Score 123; DB 4; Length 289;
Best Local Similarity 100.0%; Pred. No. 2.4e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFKDLGENFKALVL 24
DB 37 DAHKSEVAHRFKDLGENFKALVL 60

RESULT 24
AAR14178
ID AAR14178 standard; protein; 303 AA.
XX AC
XX AAR14178;
DT 19-DEC-1991 (first entry)
XX Human serum albumin lacking C-terminal fragment.
DE HSA; fusion protein; drug.
XX OS
XX Homo sapiens.
XX JF03201987-A.
XX 03-SEP-1991.
XX 29-DEC-1989; 89JP-00344701.
XX 29-DEC-1989; 89JP-00344701.
XX (TOFU ) TONEN CORP.
XX WPI; 1991-300976/41.
XX Human serum albumin fragment - where C-terminal of human serum albumin is
PT lacking and which can be combined with various drugs.
XX Claim 1; Page 1; 23pp; Japanese.
XX This sequence corresponds to amino acids 1 to 303 of mature human serum
CC albumin. The fragment lacking the C-terminal sequence can form part of a
CC fusion protein, for example with drugs. (This sequence is taken from the
CC full-length HSA sequence in EP-330451). See also AAR14179
XX SQ Sequence 303 AA;
Query Match 100.0%; Score 123; DB 2; Length 303;
Best Local Similarity 100.0%; Pred. No. 2.6e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFKDLGENFKALVL 24
DB 1 DAHKSEVAHRFKDLGENFKALVL 24

RESULT 25
AAP90387
ID AAP90387 standard; protein; 373 AA.
XX AC
XX AAP90387;
XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 01-NOV-1989 (first entry)
XX N-terminal of human serum albumin polypeptide.
DE Human serum albumin polypeptide; plasma expanders.
XX KW
XX
```

```
OS Homo sapiens; (Human).
XX EP322094-A.
XX 28-JUN-1989.
XX 25-OCT-1988; 88EP-00310000.
XX 30-OCT-1987; 87GB-00025529.
XX (DELZ ) DELTA BIOTECHNOLOGY LTD.
XX Ballance DJ, Hinchliffe E, Geisow MJ, Senior PJ;
XX WPI; 1989-186464/26.
XX New N-terminal fragments of human serum albumin - esp. useful as blood
PT plasma expanders.
XX Claim 2; Page 9; 20pp; English.
XX N-terminal portion of human serum albumin. Used as plasma expanders, or
CC as substitutes for HSA or BSA, in tissue culture media. (Updated on 25-
CC MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS
CC field)
XX SQ Sequence 373 AA;
Query Match 100.0%; Score 123; DB 1; Length 373;
Best Local Similarity 100.0%; Pred. No. 3.2e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFKDLGENFKALVL 24
DB 1 DAHKSEVAHRFKDLGENFKALVL 24

RESULT 26
AAP90389
ID AAP90389 standard; protein; 388 AA.
XX AC
XX AAP90389;
XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 01-NOV-1989 (first entry)
XX N-terminal human serum albumin polypeptide.
DE N-terminal human serum albumin polypeptide; plasma expanders.
XX KW
XX N-terminal human serum albumin polypeptide; plasma expanders.
OS Homo sapiens; (Human).
XX EP322094-A.
XX 28-JUN-1989.
XX 25-OCT-1988; 88EP-00310000.
XX 30-OCT-1987; 87GB-00025529.
XX (DELZ ) DELTA BIOTECHNOLOGY LTD.
XX Ballance DJ, Hinchliffe E, Geisow MJ, Senior PJ;
XX WPI; 1989-186464/26.
XX New N-terminal fragments of human serum albumin - esp. useful as blood
PT plasma expanders.
XX Claim 2; Page 9; 20pp; English.
XX N-terminal fragment of human serum albumin used as plasma expander, or as
```

```
CC substitutes for HSA or BSA, in tissue culture media. (Updated on 25-MAR-
CC 2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 388 AA;
    Query Match      100.0%; Score 123; DB 1; Length 388;
    Best Local Similarity 100.0%; Pred. No. 3.4e-11;
    Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAHKSEVAHRFKDLGEENFKALVL 24
    |||||
Db 1 DAHKSEVAHRFKDLGEENFKALVL 24
    |||||
RESULT 27
AAP90390
ID AAP90390 standard; protein; 389 AA.
XX
AC AAP90390;
XX
XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 01-NOV-1989 (first entry)
XX
DE N-terminal human serum albumin.
XX
XX N-terminal portion of human serum albumin; plasma expanders.
KW
XX
XX Homo sapiens; (Human).
OS
XX
XX EP322094-A.
PN
XX
XX 28-JUN-1989.
PD
XX
XX 25-OCT-1988; 88EP-00310000.
PF
XX
XX 30-OCT-1987; 87GB-00025529.
PR
XX
XX (DELZ ) DELTA BIOTECHNOLOGY LTD.
PA
XX
XX Ballance DJ, Hinchliffe E, Geisow MJ, Senior PJ;
PI
XX WPI; 1989-186464/26.
XX
XX New N-terminal fragments of human serum albumin - esp. useful as blood
XX plasma expanders.
PS
XX Claim 2; Page 9; 20pp; English.
XX
XX N-terminal portion of human serum albumin. Used to make new N-terminal
XX fragments which are used as plasma expanders, or as substitutes for HSA
XX or BSA, in tissue culture media. (Updated on 25-MAR-2003 to correct PA
XX field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
XX Sequence 390 AA;
    Query Match      100.0%; Score 123; DB 1; Length 390;
    Best Local Similarity 100.0%; Pred. No. 3.4e-11;
    Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DAHKSEVAHRFKDLGEENFKALVL 24
    |||||
Db 1 DAHKSEVAHRFKDLGEENFKALVL 24
    |||||
RESULT 29
AAU29876
ID AAU29876 standard; protein; 401 AA.
XX
XX AAU29876;
XX
XX 18-DEC-2001 (first entry)
DT
XX
XX Novel human secreted protein #367.
DE
XX
XX Human; vaccination; gene therapy; nutritional supplement;
XX stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
XX Homo sapiens.
OS
XX
XX WO200179449-A2.
PN
XX
XX 25-OCT-2001.
PD
XX
XX 16-APR-2001; 2001WO-US008656.
PF
XX
XX 18-APR-2000; 2000US-00552929.
PR
XX
XX 26-JAN-2001; 2001US-00770160.
XX
XX (HYSE-) HYSEQ INC.
PA
XX
XX Tang YT, Liu C, Drmanac RT;
PI
XX
```

DR WPI; 2001-611725/70.
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy.
XX
PS Claim 20; Page 206; 765pp; English.
XX
CC The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising the
CC nucleic acids encoding the polypeptides and cells genetically engineered
CC to express them are also useful for producing the proteins. The proteins
CC are useful in genetic vaccination, testing and therapy, and can be used
CC as nutritional supplements. They may be used to increase stem cell
CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
CC and/or nerve tissue growth or regeneration; immune suppression and/or
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
CC AAU29510-AAU3304 represent the amino acid sequences of novel human
CC secreted proteins of the invention
XX
SQ Sequence 401 AA;
Query Match 100.0%; Score 123; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 3.5e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAKHSEVAHRFKDLGLENFKALVL 24
DB 38 DAKHSEVAHRFKDLGLENFKALVL 61
RESULT 30
AAP90392
ID AAP90392 standard; protein; 407 AA.
AC AAP90392;
XX
XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 01-NOV-1989 (first entry)
XX
XX N-terminal human serum albumin.
DE Human serum albumin; mature protein; new polypeptides; plasma expanders.
XX
XX Homo sapiens; (Human).
XX
XX EP322094-A.
XX
XX 28-JUN-1989.
XX
XX 25-OCT-1988; 88EP-00310000.
XX
XX 30-OCT-1987; 87GB-00025529.
XX
XX (DELZ) DELTA BIOTECHNOLOGY LTD.
XX
XX Ballance DJ, Hinchliffe E, Geisow MJ, Senior PJ;
XX WPI; 1989-186464/26.
XX
XX New N-terminal fragments of human serum albumin - esp. useful as blood
XX plasma expanders.
PT
XX Claim 2; Page 9; 20pp; English.
PS
XX N-terminal portion of human serum albumin. Used to make plasma expanders,
CC or as substitutes for HSA or BSA, in tissue culture media. (Updated on 25

CC -MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS
CC field)
XX
SQ Sequence 407 AA;
Query Match 100.0%; Score 123; DB 1; Length 407;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAKHSEVAHRFKDLGLENFKALVL 24
DB 1 DAKHSEVAHRFKDLGLENFKALVL 24
RESULT 31
ADD32019
ID ADD32019 standard; protein; 500 AA.
XX
XX ADD32019;
AC
XX 15-JAN-2004 (first entry)
DT
XX Heterologous fusion protein related protein sequence SEQ ID NO:25.
DE
XX heterologous fusion protein;
XX heterologous fusion protein;
XX hyperglycosylated granulocyte-colony stimulating factor; G-CSF;
XX human albumin; human albumin analogue; immunoglobulin; Fc;
XX immunostimulant; protein therapy; neutrophil level;
XX insufficient circulating neutrophil level;
XX chronic congenital neutropenia.
XX
XX Synthetic.
XX
XX WO2003076567-A2.
PN
XX 18-SEP-2003.
PD
XX 21-FEB-2003; 2003WO-US003120.
PF
XX 05-MAR-2002; 2002US-0361948P.
PR
XX (ELIL) LILLY & CO ELI.
XX
XX Beals JM, Kuchibhotla U;
PI
XX WPI; 2003-902770/82.
DR
XX New heterologous fusion proteins with granulocyte-colony stimulating
XX factor activity, useful for increasing neutrophil levels and treating
XX patients with low circulating neutrophils, such as after chemotherapy or
XX in neutropenia.
XX
XX Disclosure; SEQ ID NO 25; 126pp; English.
PS
XX The present invention describes a heterologous fusion protein (I)
XX comprising a hyperglycosylated granulocyte-colony stimulating factor (G-
XX CSF) analogue fused to a polypeptide having human albumin, human albumin
XX analogues, or fragments of human albumin, or the Fc portion of an
XX immunoglobulin, an analogue of the Fc portion of an immunoglobulin, or
XX fragments of the Fc portion of an immunoglobulin. Also described: (1) a
XX heterologous fusion protein, which is the product of the expression in a
XX host cell of an exogenous DNA sequence encoding (1); (2) an isolated
XX nucleic acid sequence comprising: (a) polynucleotides encoding (1); or
XX (b) a polynucleotide, which comprises any of 15 DNA sequences each
XX comprising 1044 base pairs (see ADD31996 to ADD32010), fused to the DNA
XX encoding a protein (i.e. human albumin, human albumin analogue or
XX fragments of human albumin); (3) increasing neutrophil levels in a mammal
XX comprising the administration of (1); (4) pharmaceutical formulations
XX adapted for the treatment of patients with insufficient neutrophil levels
XX comprising any of (1); (5) a vector comprising the polynucleotide of (2);
XX (6) host cells comprising the vector of (5), or expressing at least one
XX heterologous protein; and (7) producing (1). (1) has immunostimulant
XX activity, and can be used in protein therapy. (1) can be used for

Sequence 500 AA;

Query Match 100.0%; Score 123; DB 8; Length 544;
Best Local Similarity 100.0%; Pred. No. 5e-11;
Matches 24; Conservative 0; Mismatches 0; Indels

Qy	1	DAHKSEVAH	FKD	LG	EE	NF	KAL	VL	24
Qy	25	DAHKSEVAH <td>FKD <td>LG <td>EE <td>NF <td>KAL <td>VL <td>48</td> </td></td></td></td></td></td>	FKD <td>LG <td>EE <td>NF <td>KAL <td>VL <td>48</td> </td></td></td></td></td>	LG <td>EE <td>NF <td>KAL <td>VL <td>48</td> </td></td></td></td>	EE <td>NF <td>KAL <td>VL <td>48</td> </td></td></td>	NF <td>KAL <td>VL <td>48</td> </td></td>	KAL <td>VL <td>48</td> </td>	VL <td>48</td>	48

RESULT 33
AA1129877

AAU29877:

DT	18-DEC-2001	(first entry)
XX		

Novel human secreted protein #368.

KX Human; vaccination; gene therapy; nutritional supplement;
 KX stem cell proliferation; haematopoiesis; nerve tissue reg
 KX immune suppression; immune stimulation; anti-inflammatory
 KX

KW
stem cell pro
immune suppre
KW

XX Homo sapiens

XX
DN
W0200179449-A2

25-OCT-2001.

16-APR-2001: 2001WO-US008656.

18-APR-2000: 2000US-00552929.

XX
XX

XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-611725/70.

PS Claim 20: page 206; 765pp; English.

The invention relates to novel human secreted polypeptides. The

CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent

CC expressing the protein and for use in treatment of a pathology

phages carrying the genes encoding the proteins. The proteins are expressed in *E. coli* and purified. The proteins are used to express them are also useful for producing the proteins. The proteins are useful in genetic vaccination, testing and therapy, and can be used as nutritional supplements. They may be used to increase stem cell proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon and/or nerve tissue growth or regeneration; immune suppression and/or stimulation; as anti-inflammatory agents; and in treatment of leukaemias. AAU29510-AAU33304 represent the amino acid sequences of novel human secreted proteins of the invention.

secreted proteins of the invention

```
SQ Sequence 550 AA;
Query Match 100.0%; Score 123; DB 4; Length 550;
Best Local Similarity 100.0%; Pred. No. 5.1e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAKSEVAHRFKDLGGENFKALVL 24
   |||||
Db 27 DAKSEVAHRFKDLGGENFKALVL 50

RESULT 34
ABM84997
ID ABM84997 standard; protein; 571 AA.
XX
AC ABM84997;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5246.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar SR, Wang X, Au AP, Gerstin EH;
PI Stevens KA, Blanchard JL, Panzer SR, Shen EJ, Wu MC, Stuve LL;
PI Paralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtson ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
XX WPI; 2004-329368/30.
DR N-PSDB; ACN43649.
DR
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 571 AA;
```

Query Match 100.0%; Score 123; DB 8; Length 573;
 Best Local Similarity 100.0%; Pred. No. 5.3e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAKHSEVAHRFKDLGEENFKALVL 24
 Db 25 DAKHSEVAHRFKDLGEENFKALVL 48

RESULT 36
 ABM84995
 ID ABM84995 standard; protein; 573 AA.
 XX
 AC ABM84995;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:5244.
 XX
 KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
 XX
 OS Homo sapiens.
 XX
 FN WO2004023973-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 12-SEP-2003; 2003WO-US028227.
 XX
 PR 12-SEP-2002; 2002US-0410259P.
 PR 12-SEP-2002; 2002US-0410260P.
 XX
 PA (INCY-) INCYTE CORP.
 XX
 PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
 PI Harthorne TA, Suchorski MT, Altus CM, Pitts SJ, Elder LV;
 PI Mooney EM, Delegeane AM, Panzer IS, Banville SC, Reddy TP;
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
 PI Peralta CH, Anderson SB, Riboux P, Shen EJ, Wu MC, Stuve LL;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patury S, Shi X, Suarez CJ;
 XX
 DR WPI; 2004-329368/30.
 DR N-PSDB; ACN43647.
 XX
 PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 XX
 PS Claim 27; Page; 190pp; English.
 XX
 CC The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A
 CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorder, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dithp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX
 SQ Sequence 573 AA;

Query Match 100.0%; Score 123; DB 8; Length 573;

Best Local Similarity 100.0%; Pred. No. 5.3e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAKHSEVAHRFKDLGEENFKALVL 24
 Db 25 DAKHSEVAHRFKDLGEENFKALVL 48

RESULT 37
 ABG72381
 ID ABG72381 standard; protein; 584 AA.
 XX
 AC ABG72381;
 XX
 DT 10-FEB-2003 (first entry)
 XX
 DE Mature human serum albumin #2.
 XX
 KW Human; serum albumin; HSA; cancer; cytostatic; breast cancer;
 KW prostate cancer; anti-proliferative.
 XX
 OS Homo sapiens.
 XX
 FN Key Location/Qualifiers
 FT Misc-difference 241..242
 FT /note= "Encoded by GTCCACAG"
 XX
 PN US2002123080-A1.
 XX
 PD 05-SEP-2002.
 XX
 PF 14-AUG-2001; 2001US-00929552.
 XX
 PR 19-DEC-1996; 96US-00769746.
 XX
 PA (TUFT) UNIV TUFTS.
 XX
 PI Sonnenschein C, Soto AM;
 XX
 DR WPI; 2003-066789/06.
 DR N-PSDB; ABX13582.
 XX
 PT Testing human cancer cells, especially breast and prostate cancer cells,
 PT by contacting cancer cells obtained from biopsy of a patient ex vivo with
 PT antibody specific to human albumin receptor.
 XX
 PS Disclosure; Fig 2; 17pp; English.
 XX
 CC The invention relates to testing human cancer cells, comprising obtaining
 CC cancer cells from the patient and contacting the cell ex vivo with an
 CC antibody to the receptor for human albumin. The method is useful for
 CC testing human cancer cells in particular breast and prostate cancer
 CC cells. The present sequence is mature human serum albumin, HSA. The anti-
 CC proliferative effect of HSA was assayed in an experiment included in the
 CC specification
 XX
 SQ Sequence 584 AA;

Query Match 100.0%; Score 123; DB 6; Length 584;
 Best Local Similarity 100.0%; Pred. No. 5.4e-11;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAKHSEVAHRFKDLGEENFKALVL 24
 Db 1 DAKHSEVAHRFKDLGEENFKALVL 24

RESULT 38
 AAP93344
 ID AAP93344 standard; protein; 585 AA.
 XX
 AC AAP93344;
 XX

DT 25-MAR-2003 (revised)
DT 23-JUN-1990 (first entry)
XX Sequence of mature human serum albumin (HSA) as encoded by artificial
DE gene.
DE
XX
XX Mature human serum albumin; artificial gene; oligonucleotide block;
KW hypobolaemia; shock; hypoalbuminaemia.
XX
XX Homo sapiens.
OS
XX EP308381-A.
PN
XX
XX
PD 22-MAR-1989.
XX
PF 13-SEP-1988; 88EP-00850299.
XX
XX 14-SEP-1987; 87SE-00003539.
XX
XX (SKAN-) SKANDIGEN AB.
PA (MAGY) MTA SZEGEDI BIOLOG KOEZFONTI.
PA (VEPE-) VEPEX CONTRACTOR LTD.
XX
XX Aberg B, Simoncsits A, Kalan M, Csperpan I, Bajszar G;
PI
XX
XX WPI; 1989-087749/12.
DR N-PSDB; AAN90997.
DR
XX
XX Artificial gene coding for authentic human serum albumin - constructed on
PT the basis of codons most frequently used by chosen non-human host.
PT
XX
XX Disclosure; pp. 11-16; 121pp; English.
XX
XX The synthetic gene was constructed by designing a nucleotide sequence in
CC which the codons which are most frequently used by the chosen non-human
CC host were selected. In this case, it is yeast cells (Ll20; Leu2-3; 112,
CC His 3-11, 15). The synthetic HSA gene was assembled from 24
CC oligonucleotide blocks. HSA is used in therapy for the treatment of
CC hypovolaemia, shock and hypoalbuminaemia. It is also used as an additive
CC in perfusion liq. for extracorporeal circulation and as an experimental
CC antigen. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR
CC -2003 to correct PI field.)
XX
XX Sequence 585 AA;
SQ
Query Match 100.0%; Score 123; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 5.4e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAHKSEVAHRFKDLGEENFKALVL 24
Db 1 DAHKSEVAHRFKDLGEENFKALVL 24
RESULT 39
AAP90388
ID AAP90388 standard; protein; 585 AA.
XX
XX AAP90388;
AC
XX
XX 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 01-NOV-1989 (first entry)
XX
XX Mature human serum albumin polypeptide.
DE
XX
XX Human serum albumin; mature protein; new polypeptides; plasma expanders.
KW
XX
XX Homo sapiens; (Human).
OS
XX
XX EP322094-A.
PN
XX
XX 28-JUN-1989.
PD

XX 25-OCT-1988; 88EP-00310000.
PF
XX 30-OCT-1987; 87GB-00025529.
PR
XX (DELZ) DELTA BIOTECHNOLOGY LTD.
PA
XX Ballance DJ, Hinchliffe E, Geisow MJ, Senior PJ;
PI
XX WPI; 1989-186464/26.
XX
DR N-PSDB; AAN90128.
DR
XX
XX New N-terminal fragments of human serum albumin - esp. useful as blood
PT plasma expanders.
PT
XX Disclosure; Fig 2; 20pp; English.
PS
XX
XX Mature protein of human serum albumin (see corresp. AAN90128). Used to
CC make new N-terminal fragments which are used as plasma expanders, or as
CC substitutes for HSA or BSA, in tissue culture media. (Updated on 25-MAR-
CC 2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS
CC field)
XX
XX Sequence 585 AA;
SQ
Query Match 100.0%; Score 123; DB 1; Length 585;
Best Local Similarity 100.0%; Pred. No. 5.4e-11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DAHKSEVAHRFKDLGEENFKALVL 24
Db 1 DAHKSEVAHRFKDLGEENFKALVL 24
RESULT 40
AAP91422
ID AAP91422 standard; protein; 585 AA.
XX
XX AAP91422;
AC
XX 25-MAR-2003 (revised)
XX 20-DEC-1989 (first entry)
DT
XX
XX Human normal serum albumin A.
DE
XX
XX Human normal serum albumin A; pAT-pho-HSA-A; haemorrhagic shock;
KW hypoalbuminaemia.
XX
XX Homo sapiens.
OS
XX EP330451-A.
PN
XX
XX 30-AUG-1989.
PD
XX
XX 22-FEB-1989; 89EP-00301731.
PF
XX 22-FEB-1988; 88JP-00037453.
PR
XX
XX (TOFU) TOA NENRYO KOGYO KK.
PA
XX Suzuki M, Maki N, Yagi S;
PI
XX WPI; 1989-250534/35.
DR
XX
XX CDNA encoding human normal serum albumin contained in plasmid - obt'd. by
PT culturing host transformed with expression vector comprising CDNA coding
PT for albumin.
XX
XX Claim 1; Fig 3-1 to 3-5; 19pp; English.
PS
XX
XX CDNA amino acid sequence of human serum albumin A (HSA-A) which is
CC identical to that encoded by chromosomal DNA. Previous polypeptides
CC produced from CDNA have one or more amino acids which differ from those

CC of HSA-A produced from the chromosomal DNA, and may exhibit antigenicity
CC when administered to humans. The HSA-A is used to treat haemorrhagic
CC shock and hypocalbinaemia. See also AAN90600. (Updated on 25-MAR-2003 to
CC correct PI field.)

Search completed: August 19, 2005, 10:58:24
Job time : 165 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 19, 2005, 10:45:00 ; Search time 56 Seconds
(without alignments)
219.463 Million cell updates/sec

Title: US-09-846-328B-1_COPY_2_25
Perfect score: 123
Sequence: 1 DAHKEVAHRFKDLGEENFKALVL 24

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123	100.0	167	2 Q6UXK4	Q6uxk4 homo sapien
2	123	100.0	396	2 Q8IUK7	Q8Iuk7 homo sapien
3	123	100.0	609	1 ALBU_HUMAN	P02768 homo sapien
4	117	95.1	609	2 Q68DN5	Q68dns homo sapien
5	111	90.2	21	2 Q9QVAL	Q9qval rattus sp.
6	111	90.2	417	2 Q86YGO	Q86ygo homo sapien
7	110	89.4	600	1 ALBU_MACMU	Q28522 macaca mula
8	110	89.4	608	2 Q95VB7	Q95vb7 schistosoma
9	109	88.6	607	1 ALBU_BOVIN	P02769 bos taurus
10	106	86.2	608	1 ALBU_RAT	P02770 rattus norv
11	105	85.4	607	1 ALBU_SHEEP	P14639 ovis aries
12	100	81.3	607	1 ALBU_HORSE	P35747 equus cabal
13	98	79.7	205	2 Q8CG74	Q8cg74 mus musculus
14	98	79.7	608	1 ALBU_MOUSE	P07724 mus musculus
15	98	79.7	608	2 Q8C7H3	Q8c7h3 mus musculus
16	97	78.9	584	2 Q7YSG3	Q7ysg3 felis silve
17	97	78.9	605	1 ALBU_PIG	P08835 sus scrofa
18	97	78.9	607	2 Q6BNH7	Q6bnh7 sus scrofa
19	97	78.9	608	1 ALBU_FELCA	P49064 felis silve
20	97	78.9	608	2 Q6WDN9	Q6wdn9 cavia porce
21	97	78.9	609	1 ALBU_MERUN	Q35090 meriones un
22	93	75.6	40	2 Q9TRA5	Q9tra5 oryctolagus
23	93	75.6	608	1 ALBU_RABIT	P49065 oryctolagus
24	92	74.8	20	2 Q9QUX8	Q9qux8 rattus sp.
25	92	74.8	608	1 ALBU_CANFA	P49822 canis famil
26	89	72.4	30	2 Q7M3A0	Q7m3a0 tachyglossu
27	87	70.7	20	2 Q9R4X7	Q9r4x7 mycobacteri
28	87	70.7	25	2 Q9TRW8	Q9trw8 trichosurus
29	84	68.3	583	2 Q6B3Z0	Q6b3z0 elephas max
30	81	65.9	615	1 ALBU_CHICK	P19121 gallus gall
31	76	61.8	40	1 ALB1_TRASC	P81188 trachemys s

32	71	57.7	17	2 Q9TR98	Q9tr98 canis famil
33	71	57.7	30	2 Q9PRW0	Q9prw0 struthio ca
34	61	49.6	144	2 Q8E1L1	Q8e1l1 streptococc
35	61	49.6	144	2 Q8E728	Q8e728 streptococc
36	60	48.8	15	1 NF41_NAEFO	P83729 naegleria f
37	59	48.0	548	2 Q7M8S9	Q7m8s9 wolinnella s
38	58	47.2	101	1 ALBU_NEOFS	P83517 neoceratodu
39	56	45.5	576	2 Q8C7C7	Q8c7c7 mus musculu
40	53	43.1	569	2 Q6ZQ53	Q6zq53 mus musculu
41	53	43.1	952	2 Q7TT14	Q7tt14 mus musculu
42	53	43.1	1002	1 RBMC_MOUSE	Q8r4x3 mus musculu
43	53	43.1	1032	2 Q6XLI7	Q6xli7 rattus norv
44	52	42.3	112	2 Q7NUJ3	Q7nuj3 gloeobacter
45	52	42.3	384	2 Q83K42	Q83k42 shigella fl

ALIGNMENTS

RESULT 1					
Q6UXK4					
ID	Q6UXK4	PRELIMINARY;	PRT;	167 AA.	
AC	Q6UXK4;				
DT	05-JUL-2004 (Tremblrel. 27, Created)				
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)				
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)				
DE	ALB (Fragment)				
GN	ORFNames=UNQ696;				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.12933003;				
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,				
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,				
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,				
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,				
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,				
RA	Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,				
RA	Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,				
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,				
RA	Godowski P.;				
RT	"The secreted protein discovery initiative (SPDI), a large-scale				
RT	effort to identify novel human secreted and transmembrane proteins: a				
RT	bioinformatics assessment."				
RL	Genome Res. 13:2265-2270(2003).				
DR	EMBL; AY358313; AAQ89947.1; -				
DR	HSSP; P02768; IAO6.				
DR	GO; GO:0005615; C:extracellular space; IEA.				
DR	GO; GO:0005386; F:carrier activity; IEA.				
DR	GO; GO:0006810; P:transport; IEA.				
DR	InterPro; IPR00264; Serum albumin.				
DR	Pfam; PF00273; Serum albumin; 1.				
DR	PRINTS; PR00802; SERUMALBUMIN.				
DR	SMART; SM00103; ALBUMIN; 1.				
FT	NON_TER 167 167				
SQ	SEQUENCE 167 AA; 19344 MW; 70AAC3DDA754491C CRC64;				

Query Match 100.0%; Score 123; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 4.3e-10;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	DAHKEVAHRFKDLGEENFKALVL 24	
Db	25	DAHKEVAHRFKDLGEENFKALVL 48	

RESULT 2
Q8IUK7
ID Q8IUK7
AC Q8IUK7; PRELIMINARY; PRT; 396 AA.

RL The chemistry and physiology of the human plasma proteins, pp.23-40,
 RN Pergamon Press, New York (1979).
 RL [10]
 RP SEQUENCE OF 1-455 FROM N.A.
 RA TISSUE=Liver;
 RC Menaya J., Parrilla R., Ayuso M.S.;
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP SEQUENCE OF 1-26 FROM N.A.
 RX MEDLINE=86140099; PubMed=2419329;
 RA Urano Y., Watanabe K., Sakai M., Tamaoki T.;
 RL "The human albumin gene. Characterization of the 5' and 3' flanking
 RT regions and the polymorphic gene transcripts";
 RL J. Biol. Chem. 261:3244-3251(1986).
 RN [12]
 RP SEQUENCE OF 222-229.
 RX MEDLINE=76257808; PubMed=955075; DOI=10.1016/0014-5793(76)80496-6;
 RA Walker J.B.;
 RL "Lysine residue 199 of human serum albumin is modified by
 RT acetylacetic acid";
 RL FEBS Lett. 66:173-175(1976).
 RN [13]
 RP SEQUENCE OF 25-44 AND 480-499.
 RX TISSUE=Heart;
 RC MEDLINE=95203287; PubMed=7895732;
 RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
 RL "The human myocardial two-dimensional gel protein database: update
 RT 1994";
 RL Electrophoresis 15:1459-1465(1994).
 RN [14]
 RP DISULFIDE BONDS.
 RA Sabar M.A., Stockbauer P., Moravsek L., Meloun B.;
 RL "Disulfide bonds in human serum albumin";
 RL Collect. Czech. Chem. Commun. 42:564-579(1977).
 RN [15]
 RP BILIRUBIN-BINDING SITE.
 RX MEDLINE=78186630; PubMed=656055;
 RA Jacobsen C.;
 RL "Lysine residue 240 of human serum albumin is involved in high-
 RT affinity binding of bilirubin";
 RL Biochem. J. 171:453-459(1978).
 RN [16]
 RP VARIANT CANTERBURY ASN-337.
 RX MEDLINE=87157744; PubMed=3928358; DOI=10.1016/0167-4838(87)90088-4;
 RA Brennan S.O., Herbert P.;
 RL "Albumin Canterbury (313 Lys-->Asn). A point mutation in the second
 RT domain of serum albumin";
 RL Biochim. Biophys. Acta 912:191-197(1987).
 RN [17]
 RP VARIANTS NAG-2 AND NAG-3.
 RX MEDLINE=88068523; PubMed=3479777;
 RA Takahashi N., Takahashi Y., Isobe T., Putnam F.W., Fujita M.,
 RA Satoh C., Neel J.V.;
 RL "Amino acid substitutions in inherited albumin variants from
 RT Amerindian and Japanese populations";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:8001-8005(1987).
 RN [18]
 RP VARIANTS NAG-1; HIR-1; HIR-2 AND TOCHIGI.
 RX MEDLINE=89345611; PubMed=2762316;
 RA Arai K., Madison J., Huss K., Ishioka N., Satoh C., Fujita M.,
 RA Neel J.V., Sakurabayashi I., Putnam F.W.;
 RL "Point substitutions in Japanese allalbumins";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:6092-6096(1989).
 RN [19]
 RP VARIANTS MANAUS; OSAKA; NAGOYA; FUKUOKA; HONOLULU AND NEW-GUINEA.
 RX MEDLINE=90115905; PubMed=2404284;
 RA Arai K., Madison J., Shimizu A., Putnam F.W.;
 RL "Point substitutions in albumin genetic variants from Asia";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:497-501(1990).
 RN [20]
 RP DESCRIPTION OF VARIANT REDHILL.
 RX MEDLINE=90115952; PubMed=2104980;
 RA Brennan S.O., Myles T., Peach R.J., Donaldson D., George P.M.;

RT "Albumin Redhill (-1 Arg, 320 Ala-->Thr): a glycoprotein variant of
 RL human serum albumin whose precursor has an aberrant signal peptidase
 RT cleavage site";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:26-30(1990).
 RN [21]
 RP VARIANTS TORINO LYS-84; VARESE HIS-23 AND VIBO VALENTIA LYS-106.
 RX MEDLINE=91062352; PubMed=2247440;
 RA Galliano M., Minchiotti L., Porta F., Rossi A., Ferri G., Madison J.,
 RA Watkins S., Putnam F.W.;
 RL "Mutations in genetic variants of human serum albumin found in
 RT Italy";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8721-8725(1990).
 RN [22]
 RP VARIANT VENEZIA.
 RX MEDLINE=91296740; PubMed=2068071;
 RA Watkins S., Madison J., Davis E., Sakamoto Y., Galliano M.,
 RA Minchiotti L., Putnam F.W.;
 RL "A donor splice mutation and a single-base deletion produce two
 RT carboxyl-terminal variants of human serum albumin";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:5959-5963(1991).
 RN [23]
 RP VARIANTS IOWA CITY-2 VAL-25; IOWA CITY-1 VAL-389; KOMAGOME-3 HIS-23;
 RX KOMAGOME-2 ARG-152 AND KOMAGOME-1 GLU-396.
 RL MEDLINE=92052189; PubMed=1946412;
 RA Madison J., Arai K., Feld R.D., Kyle R.A., Watkins S., Davis E.,
 RA Matsuda Y.-I., Amaki I., Putnam F.W.;
 RL "Genetic variants of serum albumin in Americans and Japanese";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:9853-9857(1991).
 RN [24]
 RP VARIANT CASEBROOK ASN-518.
 RX MEDLINE=91316157; PubMed=1859851; DOI=10.1016/0925-4439(91)90023-3;
 RA Peach R.J., Brennan S.O.;
 RL "Structural characterization of a glycoprotein variant of human serum
 RT albumin: albumin Casebrook (494 Asp-->Asn)";
 RL Biochim. Biophys. Acta 1097:49-54(1991).
 RN [25]
 RP VARIANTS SONDRIO LYS-357 AND PARIS-2 ASN-587.
 RX MEDLINE=92130239; PubMed=1347703; DOI=10.1016/0167-4838(92)90207-T;
 RA Minchiotti L., Galliano M., Stoppini M., Ferri G., Crespeau H.,
 RA Rochu D., Porta F.;
 RL "Two allalbumins with identical electrophoretic mobility are produced
 RT Query Match 100.0%; Score 123; DB 1; Length 609;
 Best Local Similarity 100.0%; Pred. No. 1.7e-09;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DAHKSEVAHFRFKDLGSENFKALVL 24
 |||||
 Db 25 DAHKSEVAHFRFKDLGSENFKALVL 48
 RESULT 4
 Q68DN5 PRELIMINARY; PRT; 609 AA.
 ID Q68DN5
 AC Q68DN5;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein DKFp779N1935.
 GN Name=DKFp779N1935;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RG The German cDNA Consortium;
 RA Bloeker H., Boecker M., Brandt P., Mewes H.W., Weil B., Amid C.,
 RA Osanger A., Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; CR749331; CAH185.1;
 DR InterPro; IPR001703; AlphaFoldProt.

```

DR InterPro: IPR000264; Serum albumin.
DR Pfam: PF00273; Serum albumin; 3.
DR PRINTS: PRO0803; AFETPROTEIN.
DR PRINTS: PRO0802; SERUMALBUMIN.
DR ProDom: PD002486; Serum_albumin; 1.
DR SMART: SM00103; ALBUMIN; 3.
DR PROSITE: PS00212; ALBUMIN; 3.
KW Hypothetical protein.
SQ SEQUENCE 609 AA; 69402 MW; 3BA3AFF17BF99E94 CRC64;

Query Match          95.1%; Score 117; DB 2; Length 609;
Best Local Similarity 95.8%; Pred. No. 1.3e-08;
Matches 23; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGEENFKALVL 24
Db 25 DAYKSEVAHRFKDLGEENFKALVL 48

RESULT 5
Q9QVAL PRELIMINARY; PRT; 21 AA.
AC Q9QVAL;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 49 kDa protein (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=93105636; PubMed=1468220;
RA Zhu L., Crouch R.K.;
RT "Albumin in the cornea is oxidized by hydrogen peroxide.";
RL Cornea 11:567-572(1992).
DR HSP; P02768; IN5U.
DR GO: GO:0005615; C:extracellular space; IEA.
DR GO: GO:0005386; F:carrier activity; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR00264; Serum albumin.
DR Pfam: PF00273; Serum_albumin; 1.
SQ SEQUENCE 21 AA; 2429 MW; 261343D7CE29FAC CRC64;

Query Match          90.2%; Score 111; DB 2; Length 21;
Best Local Similarity 100.0%; Pred. No. 2.9e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGEENFKA 21
Db 1 DAHKSEVAHRFKDLGEENFKA 21

RESULT 6
Q86YGO PRELIMINARY; PRT; 417 AA.
AC Q86YGO;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ALB protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszewski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041789; AAH41789.1; -.
DR HSP; P02768; IE7B.
DR GO: GO:0005615; C:extracellular space; IEA.
DR GO: GO:0005386; F:carrier activity; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR000264; Serum_albumin.
DR Pfam: PF00273; Serum_albumin; 2.
DR PRINTS: PRO0802; SERUMALBUMIN.
DR ProDom: PD002486; Serum_albumin; 1.
DR SMART: SM00103; ALBUMIN; 2.
DR PROSITE: PS00212; ALBUMIN; 2.
SQ SEQUENCE 417 AA; 47360 MW; 16E764833BEF4E8D CRC64;

Query Match          90.2%; Score 111; DB 2; Length 417;
Best Local Similarity 100.0%; Pred. No. 6.7e-08;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGEENFKA 21
Db 25 DAHKSEVAHRFKDLGEENFKA 45

RESULT 7
ALBU_MACMU STANDARD; PRT; 600 AA.
AC Q28522;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serum albumin precursor (Fragment).
GN Name=ALB;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93211971; PubMed=8460152;
RA Watkins S.A., Sakamoto Y., Madison J.M., Davis E.M., Smith D.G.,
RA Dwulet J., Putnam F.W.;
RT "cDNA and protein sequence of polymorphic macaque albumins that differ
in bilirubin binding.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:2409-2413(1993).
CC -!- FUNCTION: Serum albumin, the main protein of plasma, has a good
binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
hormones, bilirubin and drugs. Its main function is the regulation
of the colloidal osmotic pressure of blood.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: Belongs to the ALB/AFP/VDB family.

```


RA Patterson J.E., Geller D.M.;
RT "Bovine microsomal albumin: amino terminal sequence of bovine
RL proalbumin.";
RL Biochem. Biophys. Res. Commun. 74:1220-1226(1977).
[7]
RN
RP SEQUENCE, AND REVISIONS TO 118-119 AND 180.
RX MEDLINE=91083649; PubMed=2260975;
RA Hirayama K., Akashi S., Furuya M., Fukuhara K.-I.;
RT "Rapid confirmation and revision of the primary structure of bovine
RL serum albumin by ES/MS and Frit-FAB LC/MS.";
RL Biochem. Biophys. Res. Commun. 173:639-646(1990).
[8]
RN
RP SEQUENCE OF 25-424 AND 429-607, AND VARIANT THR-214.
RA Brown J.R.;
RT "Structure of bovine serum albumin.";
RL Fed. Proc. 34:591-591(1975).
[9]
RN
RP REVISIONS TO 190-195.
RA Brown J.R.;
RL Submitted (APR-1975) to the PIR data bank.
[10]
RN
RP SEQUENCE OF 25-64.
RX PubMed=2379503;
RA Strawich E., Glimcher M.J.;
RT "Tooth 'enamelins' identified mainly as serum proteins. Major
RL 'enamelin' is albumin.";
RL Eur. J. Biochem. 191:47-56(1990).
[11]
RN
RP SEQUENCE OF 25-41.
RX MEDLINE=88267456; PubMed=3389500;
RA Hsieh J.C., Lin F.P., Tam M.F.;
RT "Electroblotting onto glass-fiber filter from an analytical
RL isoelectrofocusing gel: a preparative method for isolating proteins
RL for N-terminal microsequencing.";
RL Anal. Biochem. 170:1-8(1988).
[12]
RN
RP SEQUENCE OF 163-172.
RX PubMed=2474509;
RA Carraway R.E., Cochran D.E., Boucher W., Mitra S.P.;
RT "Structures of histamine-releasing peptides formed by the action of
RL acid proteases on mammalian albumin(s).";
RL J. Immunol. 143:1680-1684(1989).
[13]
RN
RP SEQUENCE OF 402-433.
RX MEDLINE=82033364; PubMed=7283978;
RA Reed R.G., Putnam F.W., Peters T. Jr.;
RT "Sequence of residues 400-403 of bovine serum albumin.";
RL Biochem. J. 191:867-868(1980).
[14]
RN
RP SEQUENCE OF 437-451.
RA Vilbois F.;
RL Submitted (AUG-1998) to Swiss-Prot.
[15]
RN
RP DISULFIDE BONDS.
RA Brown J.R.;
RT "Structure of serum albumin: disulfide bridges.";
RL Fed. Proc. 33:1389-1389(1974).
CC -I- FUNCTION: Serum albumin, the main protein of plasma, has a good
CC binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
CC hormones, bilirubin and drugs. Its main function is the regulation
CC of the colloidal osmotic pressure of blood.
CC
CC -I- SUBCELLULAR LOCATION: Secreted.
CC
CC -I- TISSUE SPECIFICITY: Plasma.
CC
CC -I- ALLERGEN: Causes an allergic reaction in human.
CC
CC -I- SIMILARITY: Belongs to the ALB/APP/VDB family.
CC
CC -I- SIMILARITY: Contains 3 albumin domains.
CC
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CC -----
DR EMBL; W73993; AAA51411.1; -.
DR EMBL; X58989; CAA41735.1; -.
DR EMBL; Y17769; CAA76847.1; -.
DR EMBL; AF542068; AAN17824.1; -.
DR PIR; A38885; ABBOS.
DR HSSP; P02768; LHK1.
DR InterPro; IPR001703; Alphafetoprot.
DR InterPro; IPR000264; Serum albumin.
DR Pfam; PF00273; Serum albumin; 3.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum albumin; 1.
DR SMART; SM00103; ALBUMIN_3.
DR PROSITE; PS00212; ALBUMIN; 3.
KW Allergen; Copper; Direct protein sequencing; Lipid-binding;
KW Metal-binding; Polymorphism; Repeat; Signal.
FT SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 607 Serum albumin.
FT DOMAIN 25 204 Albumin 1.
FT DOMAIN 211 396 Albumin 2.
FT DOMAIN 403 594 Albumin 3.
FT METAL 27 27 Copper (By similarity).
FT DISULFID 77 86
FT DISULFID 99 115
FT DISULFID 114 125
FT DISULFID 147 192
FT DISULFID 191 200
FT DISULFID 223 269
FT DISULFID 268 276
FT DISULFID 288 302
FT DISULFID 301 312
FT DISULFID 339 384
FT DISULFID 383 392
FT DISULFID 415 461
FT DISULFID 460 471
FT DISULFID 484 500
FT DISULFID 499 510
FT DISULFID 537 582
FT DISULFID 581 590
FT VARIANT 214 214
FT CONFLICT 58 58 Missing (in Ref. 10).
FT CONFLICT 302 302 C -> K (in Ref. 8).
FT CONFLICT 304 305 KP -> PC (in Ref. 8).
FT CONFLICT 324 324 N -> D (in Ref. 8).
FT CONFLICT 394 395 ST -> TS (in Ref. 8).
FT CONFLICT 437 437 K -> R (in Ref. 14).
FT CONFLICT 493 494 SE -> ES (in Ref. 8).
SQ SEQUENCE 607 AA; 69293 MW; 39167DFE768585D4 CRC64;

Query Match 88.6%; Score 109; DB 1; Length 607;
Best Local Similarity 83.3%; Pred. No. 2e-07;
Matches 20; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAKSEVAHRRFKDLGSENFKALVL 24
DB 25 DTHKSEIAHRRFKDLGSEHFKGLVL 48

RESULT 10
ALBU_RAT
ID ALBU_RAT STANDARD; PRT; 608 AA.
AC P02770; P11382;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serum albumin precursor [Contains: Neurotensin-related peptide (NRP)].
GN Name=Alb;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;

RN RP SEQUENCE FROM N.A.
 RX MEDLINE=81223722; PubMed=7017712;
 RA Sargent T.D., Yang M., Bonner J.;
 RT "Nucleotide sequence of cloned rat serum albumin messenger RNA.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:243-246(1981).
 RN [2]
 RP SEQUENCE OF 1-38, AND PROCESSING.
 RX MEDLINE=77249657; PubMed=893447;
 RA Straus A.W., Bennett C.D., Donohue A.M., Rodkey J.A., Alberts A.W.;
 RT "Rat liver pre-proalbumin: complete amino acid sequence of the pre-
 piece. Analysis of the direct translation product of albumin messenger
 RNA.";
 RL J. Biol. Chem. 252:6846-6855(1977).
 RN [3]
 RP SEQUENCE OF 25-222.
 RX MEDLINE=78109429; PubMed=564345;
 RA Isemura S., Ikenaka T.;
 RT "Amino acid sequences of fragments I and II obtained by cyanogen
 bromide cleavage of rat serum albumin.";
 RL J. Biochem. 83:35-48(1978).
 RN [4]
 RP SEQUENCE OF 223-288 AND 572-608.
 RX MEDLINE=76260153; PubMed=956149;
 RA Isemura S., Ikenaka T.;
 RT "Fragmentation of rat serum albumin by cyanogen bromide cleavage and
 the amino acid sequences of four fragments.";
 RL J. Biochem. 79:1183-1196(1976).
 RN [5]
 RP SEQUENCE OF 166-174.
 RX TISSUE=Plasma;
 RA Caraway R.E., Mitra S.P., Cochrane D.E.;
 RT "Structure of a biologically active neurotensin-related peptide
 obtained from pepsin-treated albumin(s).";
 RL J. Biol. Chem. 262:5968-5973(1987).
 RN [6]
 RP COPPER-BINDING.
 RX MEDLINE=79001617; PubMed=80265;
 RA Aoyagi Y., Ikenaka T., Ichida F.;
 RT "Copper(II)-binding ability of human alpha-fetoprotein.";
 RL Cancer Res. 38:3483-3486(1978).
 CC -1- FUNCTION: Serum albumin, the main protein of plasma, has a good
 binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
 hormones, bilirubin and drugs. Its main function is the regulation
 of the colloidal osmotic pressure of blood.
 CC -1- FUNCTION: NRP regulates fat digestion, lipid absorption, and blood
 flow (potential).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Plasma.
 CC -1- SIMILARITY: Belongs to the ALB/APP/VDB family.
 CC -1- SIMILARITY: Contains 3 albumin domains.
 CC -----
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 CC -----
 CC EMBL; V01222; CAA24532.1; -.
 DR PIR; A93872; ABRTS.
 DR HSSP; P02768; 1HK1.
 DR Rat-heart-2DPAGE; P02770; -.
 DR RGD; 2085; Alb.
 DR InterPro; IPR001703; AlphaFetoprot.
 DR InterPro; IPR000264; Serum albumin.
 DR Pfam; PF00273; Serum albumin; 3.
 DR PRINTS; PR00802; SERUMALBUMIN.
 DR ProDom; PD002486; Serum albumin; 1.
 DR SMART; SM00103; ALBUMIN_3.
 DR PROSITE; PS00212; ALBUMIN; 3.

KW Copper; Direct protein sequencing; Lipid-binding; Metal-binding;
 KW Repeat; Signal.
 FT SIGNAL 1 18
 FT PROPEP 19 24
 FT CHAIN 25 608
 FT PEPTIDE 166 174
 FT DOMAIN 25 205
 FT DOMAIN 212 397
 FT DOMAIN 404 595
 FT METAL 27 27
 FT DISULFID 77 86
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 FT DISULFID 500 511
 FT DISULFID 538 583
 FT DISULFID 582 591
 FT VARIANT 262 262
 FT CONFLICT 174 174
 FT SEQUENCE 608 AA; 68718 MW; 5BB497A282411AB7 CRC64;
 SQ
 QY 1 DAKHSEVAHRFKDLGEENFKALVL 24
 DB 25 EAHKSEIAHRFKDLGEQHFKGLVL 48
 Query Match 86.2%; Score 106; DB 1; Length 608;
 Best Local Similarity 79.2%; Pred. No. 5.5e-07;
 Matches 19; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 RESULT 11
 ALBU SHEEP
 ID -ALBU SHEEP STANDARD; PRT; 607 AA.
 AC P14639;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Serum albumin precursor.
 GN Name=ALB;
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 OC NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=90098889; PubMed=2602160;
 RA Brown W.M., Dziągiewska K.M., Foreman R.C., Saunders N.R.;
 RT "Nucleotide and deduced amino acid sequence of sheep serum albumin.";
 RL Nucleic Acids Res. 17:10495-10495(1989).
 CC -1- FUNCTION: Serum albumin, the main protein of plasma, has a good
 binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
 hormones, bilirubin and drugs. Its main function is the regulation
 of the colloidal osmotic pressure of blood.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Plasma.
 CC -1- SIMILARITY: Belongs to the ALB/APP/VDB family.
 CC -1- SIMILARITY: Contains 3 albumin domains.
 CC -----
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CC or send an email to license@isb-sib.ch).

DR	EMBL; X17055; CAA34903.1; -.	
DR	PIR; S06936; ABSHS.	
DR	HSP; P02768; 1HK1.	
DR	InterPro; IPR001703; Alphafetoprot.	
DR	InterPro; IPR000264; Serum albumin.	
DR	Pfam; PF00273; Serum albumin; 3.	
DR	PRINTS; PR00802; SERUMALBUMIN.	
DR	ProDom; PD002486; Serum albumin; 1.	
DR	SMART; SM00103; ALBUMIN; 3.	
DR	PROSITE; PS00212; ALBUMIN; 3.	
DR	Copper; Lipid-binding; Metal-binding; Repeat; Signal.	
FT	SIGNAL	1
FT	PROPEP	19
FT	CHAIN	24
FT	CHAIN	25
FT	DOMAIN	25
FT	DOMAIN	211
FT	DOMAIN	403
FT	METAL	27
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FT	DISULFID	99
FT	DISULFID	114
FT	DISULFID	147
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FT	DISULFID	223
FT	DISULFID	268
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DR	InterPro; IPR001703; Alphafetoprot.	
DR	InterPro; IPR000264; Serum albumin.	
DR	Pfam; PF00273; Serum albumin; 3.	
DR	PRINTS; PR00802; SERUMALBUMIN.	
DR	ProDom; PD002486; Serum albumin; 1.	
DR	SMART; SM00103; ALBUMIN; 3.	
DR	PROSITE; PS00212; ALBUMIN; 3.	
DR	Copper; Lipid-binding; Metal-binding; Repeat; Signal.	
FT	SIGNAL	1
FT	PROPEP	19
FT	CHAIN	24
FT	CHAIN	25
FT	DOMAIN	25
FT	DOMAIN	211
FT	DOMAIN	403
FT	METAL	27
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FT	DISULFID	99
FT	DISULFID	114
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FT	DISULFID	191
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FT	DISULFID	537
FT	DISULFID	582
FT	DISULFID	581
FT	SEQUENCE	607
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DR	HSP; P02768; 1HK1.	
DR	InterPro; IPR001703; Alphafetoprot.	
DR	InterPro; IPR000264; Serum albumin.	
DR	Pfam; PF00273; Serum albumin; 3.	
DR	PRINTS; PR00802; SERUMALBUMIN.	
DR	ProDom; PD002486; Serum albumin; 1.	
DR	SMART; SM00103; ALBUMIN; 3.	
DR	PROSITE; PS00212; ALBUMIN; 3.	
DR	Copper; Lipid-binding; Metal-binding; Repeat; Signal.	
FT	SIGNAL	1
FT	PROPEP	19
FT	CHAIN	24
FT	CHAIN	25
FT	DOMAIN	25
FT	DOMAIN	211
FT	DOMAIN	403
FT	METAL	27
FT	DISULFID	77
FT	DISULFID	99
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FT	DISULFID	147
FT	DISULFID	192
FT	DISULFID	200
FT	DISULFID	223
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FT	DISULFID	276
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FT	DISULFID	461
FT	DISULFID	471
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FT	DISULFID	500
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FT	DISULFID	537
FT	DISULFID	582
FT	DISULFID	581
FT	SEQUENCE	607
DR	EMBL; X17055; CAA34903.1; -.	
DR	PIR; S06936; ABSHS.	
DR	HSP; P02768; 1HK1.	
DR	InterPro; IPR001703; Alphafetoprot.	
DR	InterPro; IPR000264; Serum albumin.	
DR	Pfam; PF00273; Serum albumin; 3.	
DR	PRINTS; PR00802; SERUMALBUMIN.	
DR	ProDom; PD002486; Serum albumin; 1.	
DR	SMART; SM00103; ALBUMIN; 3.	
DR	PROSITE; PS00212; ALBUMIN; 3.	
DR	Copper; Lipid-binding; Metal-binding; Repeat; Signal.	
FT	SIGNAL	1
FT	PROPEP	19
FT	CHAIN	24
FT	CHAIN	25
FT	DOMAIN	25
FT	DOMAIN	211
FT	DOMAIN	403
FT	METAL	27
FT	DISULFID	77
FT	DISULFID	99
FT	DISULFID	115
FT	DISULFID	125
FT	DISUL	

```

binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
hormones, bilirubin and drugs. Its main function is the regulation
of the colloidal osmotic pressure of blood.
-1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: Plasma.
-1- ALLERGEN: Causes an allergic reaction in human. Binds IgE.
-1- SIMILARITY: Belongs to the ALB/AFP/VDB family.
-1- SIMILARITY: Contains 3 albumin domains.
-----
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EMBL; X74045; CAAS2194.1; -.
PIR; S34053; ABHOS.
HSP; P02768; IHK1.
InterPro; IPR000264; Serum albumin.
Pfam; PF00273; Serum albumin; 3.
PRINTS; PR00802; SERUMALBUMIN.
ProDom; PD002486; Serum_albumin; 1.
SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
Allergen; Copper; Lipid-binding; Metal-binding; Repeat; Signal.
FT SIGNAL 1 18 By similarity.
FT PROPEP 19 24 By similarity.
FT CHAIN 25 607 Serum albumin.
FT DOMAIN 25 204 Albumin 1.
FT DOMAIN 211 396 Albumin 2.
FT DOMAIN 403 594 Albumin 3.
FT METAL 27 27 Copper (By similarity).
FT DISULFID 77 86
FT DISULFID 99 115
FT DISULFID 114 125
FT DISULFID 147 192
FT DISULFID 191 200
FT DISULFID 223 269
FT DISULFID 268 276
FT DISULFID 288 302
FT DISULFID 301 312
FT DISULFID 339 384
FT DISULFID 383 392
FT DISULFID 415 461
FT DISULFID 460 471
FT DISULFID 484 500
FT DISULFID 499 510
FT DISULFID 537 582
FT DISULFID 581 590
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Query Match 81.3%; Score 100; DB 1; Length 607;
Best Local Similarity 75.0%; Pred. No. 4.2e-06;
Matches 18; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDIGHENFKALVL 24
| | | | | | | | | | | | | | | |
Db 25 DTHKSEIAHRFNDLGEKHFKGLVL 48

RESULT 13
Q8CG74 PRELIMINARY; PRT; 205 AA.
ID Q8CG74 AC
AC Q8CG74;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Albumin (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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DR EMBL; M16111; AAA37190.1; -.
DR EMBL; X13060; CAA31458.1; -.
DR PIR; A05139; A05139.
DR HSP; P02768; 1HK1.
DR SWISS-2DPAGE; P07724; MOUSE.
DR MGD; MGI:87991; Alb1.
DR InterPro; IPR001703; Alphafetoprot.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; Serum_albumin; 3.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR PROSITE; PS00212; ALBUMIN; 3.
KW Copper; Direct protein sequencing; Lipid-binding; Metal-binding;
KW Repeat; Signal.
FT SIGNAL 1 18 By similarity.
FT PROPEP 19 24
FT CHAIN 25 608 Serum albumin.
FT DOMAIN 25 205 Albumin 1.
FT DOMAIN 212 397 Albumin 2.
FT DOMAIN 404 595 Albumin 3.
FT METAL 27 27 Copper.
FT DISULFID 77 86 By similarity.
FT DISULFID 99 115 By similarity.
FT DISULFID 114 125 By similarity.
FT DISULFID 148 193 By similarity.
FT DISULFID 192 201 By similarity.
FT DISULFID 224 270 By similarity.
FT DISULFID 269 277 By similarity.
FT DISULFID 289 303 By similarity.
FT DISULFID 302 313 By similarity.
FT DISULFID 340 385 By similarity.
FT DISULFID 384 393 By similarity.
FT DISULFID 416 462 By similarity.
FT DISULFID 461 472 By similarity.
FT DISULFID 485 501 By similarity.
FT DISULFID 500 511 By similarity.
FT DISULFID 538 583 By similarity.
FT DISULFID 582 591 By similarity.
FT CONFLICT 27 37 H -> D (in Ref. 6).
FT CONFLICT 33 33 H -> D (in Ref. 6).
FT CONFLICT 41 41 Q -> I (in Ref. 6).
SQ SEQUENCE 608 AA; 68692 MW; 292F7C7BED3A61B4 CRC64;

Query Match 79.7%; Score 98; DB 1; Length 608;
Best Local Similarity 70.8%; Pred. No. 8.4e-06;
Matches 17; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAKHSEVAHRFKDLGEENFKALVL 24
DB 25 EAHKSEIHAHYNDLGEQHFGLVL 48

RESULT 15
Q8C7H3 PRELIMINARY; PRT; 608 AA.
AC Q8C7H3
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus adult male liver tumor cDNA, RIKEN full-length enriched
DE library, clone:C730030P03 product:albumin 1, full insert
DE sequence.
GN Name=Albi;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
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RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Hayada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Liver;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK050248; BAC34145.1; -.
DR HSP; P02768; 1HK1.
DR MGD; MGI:87991; Alb1.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR001703; Alphafetoprot.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; Serum_albumin; 3.
DR PRINTS; PR00803; AFETOPROTEIN.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
SQ SEQUENCE 608 AA; 68722 MW; 292F600EED3A61B4 CRC64;

Query Match 79.7%; Score 98; DB 2; Length 608;
Best Local Similarity 70.8%; Pred. No. 8.4e-06;
Matches 17; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAKHSEVAHRFKDLGEENFKALVL 24
```



```
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY663543; AAT98610.1; -.
DR InterPro: IPR000264; Serum_albumin.
DR Pfam: PF00273; Serum_albumin; 3.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
SQ SEQUENCE 607 AA; 69691 MW; 788DA13543CA99D8 CRC64;

Query Match      78.9%; Score 97; DB 2; Length 607;
Best Local Similarity 75.0%; Pred. No. 1.2e-05;
Matches 18; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAKSEVAHRFKDLGEENFKALVL 24
Db 25 DTYKSEIAHRFNDLGEHPRGLVL 48

RESULT 19
ALBU_FELCA STANDARD; PRT; 608 AA.
AC P49064;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serum albumin precursor (Allergen Fel d 2).
GN Name:ALB;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxId=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96194824; PubMed=8647469; DOI=10.1016/0378-1119(95)00851-9;
RA Hilger C., Grigioni F., Kohnen M., Hentges F.;
RT "Sequence of the gene encoding cat (Felis domesticus) serum albumin.";
RL Gene 169:295-296(1996).
CC -!- FUNCTION: Serum albumin, the main protein of plasma, has a good
CC binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
CC hormones, bilirubin and drugs. Its main function is the regulation
CC of the colloidal osmotic pressure of blood.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- ALLERGEN: Causes an allergic reaction in human.
CC -!- SIMILARITY: Belongs to the ALB/AFP/VDB family.
CC -!- SIMILARITY: Contains 3 albumin domains.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: X84842; CAA59279.1; -.
DR PIR: JC4660; S57632.
DR HSPSP; P02768; IE7B.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; Serum_albumin; 3.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
DR Allergen; Copper; Lipid-binding; Metal-binding; Repeat; Signal.
FT SIGNAL 1 18
FT PROPEP 19 24 By similarity.
FT CHAIN 25 608 Serum_albumin.
FT DOMAIN 25 205 Albumin 1.
FT DOMAIN 212 397 Albumin 2.
FT DOMAIN 404 595 Albumin 3.
FT METAL 27 27 Copper.
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FT DISULFID 77 86 By similarity.
FT DISULFID 99 115 By similarity.
FT DISULFID 114 125 By similarity.
FT DISULFID 148 193 By similarity.
FT DISULFID 192 201 By similarity.
FT DISULFID 224 270 By similarity.
FT DISULFID 269 277 By similarity.
FT DISULFID 289 303 By similarity.
FT DISULFID 302 313 By similarity.
FT DISULFID 340 385 By similarity.
FT DISULFID 384 393 By similarity.
FT DISULFID 416 462 By similarity.
FT DISULFID 461 472 By similarity.
FT DISULFID 485 501 By similarity.
FT DISULFID 500 511 By similarity.
FT DISULFID 538 583 By similarity.
FT DISULFID 582 591 By similarity.
SQ SEQUENCE 608 AA; 68659 MW; 07B629CAC5F60E5F CRC64;

Query Match      78.9%; Score 97; DB 1; Length 608;
Best Local Similarity 70.8%; Pred. No. 1.2e-05;
Matches 17; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAKSEVAHRFKDLGEENFKALVL 24
Db 25 EAHKSEIAHRFNDLGEHPRGLVL 48

RESULT 20
Q6WDN9 PRELIMINARY; PRT; 608 AA.
AC Q6WDN9;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Preproalbumin precursor.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxId=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Mihaylova-Todorova S., Choe S.M., Westfall D.P.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY294645; RAQ20088.1; -.
DR HSSP; P02768; IAO6.
DR GO; GO:0005615; C:extracellular space; IEA.
DR GO; GO:0005386; F:carrier activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001703; Alphafetoprot.
DR InterPro; IPR000264; Serum_albumin.
DR Pfam; PF00273; Serum_albumin; 3.
DR PRINTS; PR00803; AFETOPROTEIN.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
KW Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 25 608 albumin.
SQ SEQUENCE 608 AA; 68889 MW; BBD510A78D0261BA CRC64;

Query Match      78.9%; Score 97; DB 2; Length 608;
Best Local Similarity 75.0%; Pred. No. 1.2e-05;
Matches 18; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAKSEVAHRFKDLGEENFKALVL 24
Db 25 EAHKSEIAHRFNDLGEHPRGLVL 48

RESULT 21
```

ALBU MERUN STANDARD; PRT; 609 AA.

AC Q3509; 1998 (Rel. 36, Created)

DT 15-JUN-1998 (Rel. 36, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Serum albumin precursor.

GN Name=ALB;

OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;

OC Meriones.

OX NCBI_TaxID=10047;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MGS IDR; TISSUE=Liver;

RX MEDLINE=98116663; PubMed=9455485;

RA Yoshida K., Seto-Onahima A., Sinohara H.;

RT "Sequencing of cDNA encoding serum albumin and its extrahepatic synthesis in the Mongolian gerbil, Meriones unguiculatus.";

RL DNA Res 4:351-354(1997)

CC -!- FUNCTION: Serum albumin, the main protein of plasma, has a good binding capacity for water, Ca(2+), Na(+), K(+), fatty acids, hormones, bilirubin and drugs. Its main function is the regulation of the colloidal osmotic pressure of blood.

CC -!- TISSUE SPECIFICITY: Plasma.

CC -!- SIMILARITY: Belongs to the ALB/APP/VDB family.

CC -!- SIMILARITY: Contains 3 albumin domains.

CC -----

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CC -----

CC EMBL; AB006197; BAA21765.1; --

DR PIR; JCS838; JCS838.

DR HSSP; P02768; 1E7B.

DR InterPro; IPR001703; Alphafetoprot.

DR InterPro; IPR00264; Serum albumin.

DR Pfam; PF00273; Serum albumin; 3.

DR PRINTS; PR00802; SERUMALBUMIN.

DR ProDom; PD002486; Serum albumin; 1.

DR SMART; SM00103; ALBUMIN; 3.

DR PROSITE; PS00212; ALBUMIN; 3.

DR Copper; Lipid-binding; Metal-binding; Repeat; Signal.

FT SIGNAL 1 18

FT PROPEP 19 24 By similarity.

FT CHAIN 25 609 Serum albumin.

FT DOMAIN 25 206 Albumin 1.

FT DOMAIN 213 398 Albumin 2.

FT DOMAIN 405 596 Albumin 3.

FT METAL 28 28 Copper.

FT DISULFID 28 87 By similarity.

FT DISULFID 100 116 By similarity.

FT DISULFID 115 126 By similarity.

FT DISULFID 149 194 By similarity.

FT DISULFID 193 202 By similarity.

FT DISULFID 225 271 By similarity.

FT DISULFID 270 278 By similarity.

FT DISULFID 290 304 By similarity.

FT DISULFID 303 314 By similarity.

FT DISULFID 341 386 By similarity.

FT DISULFID 385 394 By similarity.

FT DISULFID 417 463 By similarity.

FT DISULFID 462 473 By similarity.

FT DISULFID 486 502 By similarity.

FT DISULFID 501 512 By similarity.

FT DISULFID 539 584 By similarity.

FT DISULFID 583 592 By similarity.

SQ SEQUENCE 609 AA; 68940 MW; 9CA5F97F67E7E7F1A48 CRC64;

Query Match 78.9%; Score 97; DB 1; Length 609;

Best Local Similarity 78.3%; Pred. No. 1.2e-05;

Matches 18; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 AHKSEVAHRFKDLGEENFKALVL 24
:||||:||||:||||:||||:||||

DB 27 AHKSEIAHRYKDLGEKYFKGLVL 49
:||||:||||:||||:||||:||||

RESULT 22

Q9TRAS PRELIMINARY; PRT; 40 AA.

ID AC Q9TRAS

AC Q9TRAS5;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Antagonist protein (Fragment).

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN [1]

RP SEQUENCE.

RX MEDLINE=94359514; PubMed=8078511;

RA Xu A., Narayanan N.;

RT "Purification, amino-terminal sequence and functional properties of a 64 kDa cytosolic protein from heart muscle capable of modulating calcium transport across the sarcoplasmic reticulum in vitro.";

RL Mol. Cell. Biochem. 132:7-14(1994).

DR HSSP; P02768; 1NSU.

DR GO; GO:0005615; C:extracellular space; IEA.

DR GO; GO:0005386; F:carrier activity; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR00264; Serum albumin.

DR Pfam; PF00273; Serum_albumin; 1.

SQ SEQUENCE 40 AA; 4694 MW; BA7E0B69C6CB859C CRC64;

Query Match 75.6%; Score 93; DB 2; Length 40;

Best Local Similarity 70.8%; Pred. No. 2.6e-06;

Matches 17; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFKDLGEENFKALVL 24
:||||:||||:||||:||||:||||

DB 1 EAHKSEIAHRYFNDVGEHFGLVL 24
:||||:||||:||||:||||:||||

RESULT 23

ALBU RABIT STANDARD; PRT; 608 AA.

ID AC P49055;

DT 01-FEB-1996 (Rel. 33, Created)

DT 29-MAR-2004 (Rel. 43, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Serum albumin precursor.

GN Name=ALB;

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=New Zealand white; TISSUE=Liver;

RX MEDLINE=97275135; PubMed=9129029;

RA Syed S., Schuyler P.D., Kulczycky M., Sheffield W.P.;

RT "Potent antithrombin activity and delayed clearance from the circulation characterize recombinant hirudin genetically fused to albumin.";

RL Blood 89:3243-3252(1997).

RN [2]

RP REVISIONS TO 322-323 AND 506-507.

RA Sheffield W.P.;

```
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: Serum albumin, the main protein of plasma, has a good
CC binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
CC hormones, bilirubin and drugs. Its main function is the regulation
CC of the colloidal osmotic pressure of blood.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Plasma.
CC -|- SIMILARITY: Belongs to the ALB/AFP/VDB family.
CC -|- SIMILARITY: Contains 3 albumin domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U18344; RA058347.2; -.
DR HSPSP; P02768; I27B.
DR InterPro; IPR000264; Serum albumin.
DR Pfam; PF00273; Serum_albumin; 3.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
KW Copper; Lipid-binding; Metal-binding; Repeat; Signal.
FT SIGNAL 1 18 By similarity.
FT PROPEP 19 24 By similarity.
FT CHAIN 25 608 Serum albumin.
FT DOMAIN 25 205 Albumin 1.
FT DOMAIN 212 397 Albumin 2.
FT DOMAIN 404 595 Albumin 3.
FT METAL 27 27 Copper.
FT DISULFID 77 86 By similarity.
FT DISULFID 99 115 By similarity.
FT DISULFID 114 125 By similarity.
FT DISULFID 148 193 By similarity.
FT DISULFID 192 201 By similarity.
FT DISULFID 224 270 By similarity.
FT DISULFID 269 277 By similarity.
FT DISULFID 289 303 By similarity.
FT DISULFID 302 313 By similarity.
FT DISULFID 340 385 By similarity.
FT DISULFID 384 393 By similarity.
FT DISULFID 416 462 By similarity.
FT DISULFID 461 472 By similarity.
FT DISULFID 485 501 By similarity.
FT DISULFID 500 511 By similarity.
FT DISULFID 538 583 By similarity.
FT DISULFID 582 591 By similarity.
SQ SEQUENCE 608 AA; 68909 MW; 9EECAFDA86B1EF09 CRC64;

Query Match 75.68; Score 93; DB 1; Length 608;
Best Local Similarity 70.88; Pred.No. 4.6e-05;
Matches 17; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFKDLGEENFKALVL 24
Db 25 EAHKSEIAHRFNDVGEHFGVLVL 48
:|||||:|||||:|||||:|||||:

RESULT 24
Q9QUX8 PRELIMINARY; PRT; 20 AA.
AC Q9QUX8
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 70 kDa seizure activity-linked albumin-like glycoprotein (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
```

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OX NCBI_TaxID=10118;
RN [1]_
RP SEQUENCE.
RX MEDLINE=96087830; PubMed=8597647;
RA Onoaka M., Inai S., Isobe T., Yen C.T., Watanabe K.;
RT "Purification and characterization of a novel 70-kDa brain protein
RT associated with seizure activities.";
RL Neurochem. Res. 20:901-905(1995).
DR HSPSP; P02768; I27B.
SQ SEQUENCE 20 AA; 2381 MW; 534A23C0F9F70F7D CRC64;

Query Match 74.88; Score 92; DB 2; Length 20;
Best Local Similarity 80.0%; Pred.No. 1.8e-06;
Matches 16; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAHKSEVAHRFKDLGEENFK 20
Db 1 EAHKSEIAHRFNDVGEHFGVL 20
:|||||:|||||:|||||:|||||:

RESULT 25
ALBU_CANFA STANDARD; PRT; 608 AA.
ID ALBU CANFA
AC P49822; O77705; Q9TS24;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serum albumin precursor (Allergen Can f 3).
GN Name=ALB;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=Beagle; TISSUE=Liver;
RA Hilger C.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]_
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20148667; PubMed=10669848; DOI=10.1016/S0091-6749(00)90077-0;
RA Pandjaitan B., Swoboda I., Brandesky-Pichler F., Rumpold H.,
RA Valenta R., Spitzauer S.;
RT "Escherichia coli expression and purification of recombinant dog
RT albumin, a cross-reactive animal allergen.";
RL J. Allergy Clin. Immunol. 105:279-285(2000).
RN [3]_
RP SEQUENCE OF 25-48.
RX MEDLINE=75011422; PubMed=4414013;
RA Dixon J.W., Sarkar B.;
RT "Isolation, amino acid sequence and copper(II)-binding properties of
RT peptide (1-24) of dog serum albumin.";
RL J. Biol. Chem. 249:5872-5877(1974).
RN [4]_
RP SEQUENCE OF 25-38.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
RN [5]_
RP SEQUENCE OF 215-478 FROM N.A.
RC TISSUE=Salivary gland;
RX MEDLINE=94201492; PubMed=7512102;
RA Spitzauer S., Schweizer C., Sperr W.R., Pandjaitan B., Valent P.,
RA Muehl S., Ebner C., Scheiner O., Kraft D., Rumpold H.;
RT "Molecular characterization of dog albumin as a cross-reactive
RT allergen.";
RL J. Allergy Clin. Immunol. 93:614-627(1994).
CC -|- FUNCTION: Serum albumin, the main protein of plasma, has a good
CC binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
```



```

DE Serum albumin (Fragment).
OS Trichosurus vulpecula (Brush-tailed possum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
OX NCBI_TaxID=9337;
RN [1]
RP SEQUENCE.
RA MEDLINE=91330574; PubMed=1868684;
RX Grigor M.R., Bennett B.L., Carne A., Cowan P.E.;
RT "When proteins of the common brushtail possum (Trichosurus vulpecula):
RT isolation, characterization and changes in concentration in milk
RT during lactation of transferrin, alpha-lactalbumin and serum
RT albumin.";
RL Comp. Biochem. Physiol. 98B:451-459 (1991).
DR HSP; P02768; I09X.
DR GO: GO:0005615; C:extracellular space; IEA.
DR GO: GO:0005386; F:carrier activity; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR000264; Serum albumin.
DR Pfam: PF00273; Serum_albumin; 1.
FT NON_TER 1
FT NON_TER 25
SQ SEQUENCE 25 AA; 2813 MW; FD4D08B2260C67F2 CRC64;

Query Match 70.7%; Score 87; DB 2; Length 25;
Best Local Similarity 75.0%; Pred. No. 1.2e-05;
Matches 18; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAKHSEVAHRFKDLGNEENFKALVL 24
DB 1 DAPKSEVAKRYDLDGKNVKALVL 24

RESULT 29
Q6B3Z0 PRELIMINARY; PRT; 583 AA.
ID Q6B3Z0
AC Q6B3Z0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Serum albumin (Fragment).
GN Name=ESA;
OS Elephas maximus (Indian elephant).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Proboscidea; Elephantidae; Elephas.
OX NCBI_TaxID=9783;
RN [1]
RP SEQUENCE FROM N.A.
RA Lazar J., Rasmussen B., Greenwood D.R., Bang I.-S., Prestwich G.D.;
RT "Elephant Albumin: A Multi-purpose Pheromone Shuttle.";
RL Chem. Biol. 0:0-0 (2004).
DR EMBL; AY684122; AAT90502.1; -.
DR GO: GO:0005615; C:extracellular space; IEA.
DR GO: GO:0005386; F:carrier activity; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR000264; Serum albumin.
DR Pfam: PF00273; Serum_albumin; 3.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
FT NON_TER 1
FT NON_TER 583 AA; 65767 MW; 4EC031C2ECBB9141 CRC64;

Query Match 68.3%; Score 84; DB 2; Length 583;
Best Local Similarity 68.2%; Pred. No. 0.00094;
Matches 15; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 HKSEVAHRFKDLGNEENFKALVL 24
DB 1 YKSEIAHRYKDLGSDLPKGLLL 22

RESULT 30
ALBU_CHICK STANDARD; PRT; 615 AA.
ID ALBU_CHICK
AC P19121;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serum albumin precursor (Alpha-livetin) (Allergen Gal d 5).
GN Name=ALB;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Caseady A.I., Salkild C.K., Baverstock P., Wallace J.C.;
RL Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-28 FROM N.A.
RX MEDLINE=83161037; PubMed=6187737;
RA Hache R.J.G., Wiskocil R., Vasa M., Roy R.N., Lau P.C.K., Deeley R.G.;
RT "The 5' noncoding and flanking regions of the avian very low density
RT apolipoprotein II and serum albumin genes. Homologies with the egg
RT white protein genes.";
RL J. Biol. Chem. 258:4556-4564 (1983).
RN [3]
RP SEQUENCE OF 19-30.
RX MEDLINE=78019943; PubMed=911327;
RA Rosen A.M., Geller D.M.;
RT "Chicken microsomal albumin: amino terminal sequence of chicken
RT proalbumin.";
RL Biochem. Biophys. Res. Commun. 78:1060-1066 (1977).
RN [4]
RP ALLERGENIC PROPERTIES.
RX MEDLINE=21381307; PubMed=11488669;
RA Quirce S., Maranon F., Umpierrez A., de las Heras M.,
RA Fernandez-Caldas E., Sastre J.;
RT "Chicken serum albumin (Gal d 5*) is a partially heat-labile inhalant
RT and food allergen implicated in the bird-egg syndrome.";
RL Allergy 56:754-762 (2001).
CC -!- FUNCTION: Serum albumin, the main protein of plasma, has a good
CC binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,
CC hormones, bilirubin and drugs. Its main function is the regulation
CC of the colloidal osmotic pressure of blood.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- ALLERGEN: Causes an allergic reaction in human. Binds IgE.
CC Partially heat-labile allergen that may cause both respiratory and
CC food-allergy symptoms in patients with the bird-egg syndrome.
CC -!- SIMILARITY: Belongs to the ALB/AFP/VDB family.
CC -!- SIMILARITY: Contains 3 albumin domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
DR EMBL; X60688; CAA43098.1; -.
DR EMBL; V00381; CAA23680.1; -.
DR PIR; S15571; ABCHS.
DR HSP; P02768; 1HK1.
DR InterPro: IPR001703; Alphafetoprot.
DR InterPro: IPR000264; Serum albumin.
DR Pfam: PF00273; Serum_albumin; 3.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum_albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.

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Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 HKSEVAHRFKDGLGEENFKALVL 24
Db 4 HKSEIAHRYNDLKEETDKAVXM 25

RESULT 34
Q8E1L1 PRELIMINARY; PRT; 144 AA.
AC Q8E1L1;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Transcriptional regulator, MarR family.
GN OrderedLocNames=SAG0343;
OS Streptococcus agalactiae (serotype V).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2603 V/R / Serotype V;
RX MEDLINE=2222988; PubMed=12200547; DOI=10.1073/pnas.182380799;
RA Tettelin H., Maignani V., Cieslewicz M.J., Eisen J.A., Peterson S.N.,
RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
RA Radune D., Fedorova N.B., Scanlan D., Khouri H.M., Mulligan S.,
RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
RA Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
CC -!- SIMILARITY: Contains 1 HTH marR-type DNA-binding domain.
DR EMBL; AE014207; AAM99249.1; -.
DR TIGR; SAG0343; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000835; HTH_MarR.
DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
DR Pfam; PF01047; MarR; 1.
DR PRINTS; PR00598; HTHMARR.
KW Complete proteome; DNA-binding; Transcription;
KW Transcription regulation.
SQ SEQUENCE 144 AA; 16656 MW; 465EAE2AB8F8DB34 CRC64;

Query Match 49.6%; Score 61; DB 2; Length 144;
Best Local Similarity 60.0%; Pred. No. 0.55;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 HKSEVAHRFKDGLGEENFKAL 22
Db 110 HKSMVSHIEDLGEEDIKML 129

RESULT 35
Q8E728 PRELIMINARY; PRT; 144 AA.
AC Q8E728;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein gbs0330.
GN OrderedLocNames=gbs0330;
OS Streptococcus agalactiae (serotype III).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=216495;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEM316 / Serotype III;
RX MEDLINE=22242508; PubMed=12354221;
RA Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangoul L.,
RA Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
RA Kunat F.;
RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
RT invasive neonatal disease.";
RL Mol. Microbiol. 45:1499-1513(2002).
CC -!- SIMILARITY: Contains 1 HTH marR-type DNA-binding domain.
DR EMBL; AL766844; CAD45975.1; -.
DR Sagalict; gbs0330; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR000835; HTH_MarR.
DR InterPro; IPR009058; Wing_hlx_DNA_bnd.
DR Pfam; PF01047; MarR; 1.
DR PRINTS; PR00598; HTHMARR.
DR SMART; SM00347; HTH_MARR; 1.
KW Complete proteome; DNA-binding; Transcription;
KW Transcription regulation.
SQ SEQUENCE 144 AA; 16656 MW; 465EAE2AB8F8DB34 CRC64;

Query Match 49.6%; Score 61; DB 2; Length 144;
Best Local Similarity 60.0%; Pred. No. 0.55;
Matches 12; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 HKSEVAHRFKDGLGEENFKAL 22
Db 110 HKSMVSHIEDLGEEDIKML 129

RESULT 36
NF41 NAEFO STANDARD; PRT; 15 AA.
ID NF41 NAEFO
AC P83729;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein NF041 from 2D-PAGE (Fragment).
OS Naegleria fowleri.
OC Eukaryota; Heterolobosea; Schizopyrenida; Vahlkampfiidae; Naegleria.
OX NCBI_TaxID=5763;
RN [1]
RP SEQUENCE.
RC STRAIN=Nf 66;
RA Omura M., Furushima-Shimogawara R., Izumiya S., Endo T.;
RT "Comparative study of protein profiles on pathogenic and nonpathogenic
RT Naegleria species by 2D-PAGE.";
RL J. Eukaryot. Microbiol. 0:0-0(2004).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.9, its MW is: 47.0 kDa.
KW Direct protein sequencing.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1704 MW; C70F7D308AEC51B9 CRC64;

Query Match 48.8%; Score 60; DB 1; Length 15;
Best Local Similarity 73.3%; Pred. No. 0.071;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAKKSEVAHRFKDLG 15
Db 1 DTHKSEIAHRQPDLG 15

RESULT 37
Q7M8S9 PRELIMINARY; PRT; 548 AA.
ID Q7M8S9
AC Q7M8S9;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

```

DE	PUTATIVE TWO-COMPONENT SENSOR.
GN	OrderedLocusNames=WS1436;
QS	Wolinella succinogenes.
OC	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC	Helicobacteraceae; Wolinella.
OX	NCBI_TaxID=844;
[1]	
RN	SEQUENCE FROM N.A.
RP	STRAIN=DSMZ 1740;
RC	MEDLINE=22982897; PubMed=1450908; DOI=10.1073/pnas.1932838100;
RA	Baar C., Espinger M., Raddatz G., Simon J., Lanz C., Kimmek O.,
RA	Nandakumar K., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
RA	Meyer F., Ledrer H., Schuster S.C.;
RT	"Complete genome sequence and analysis of Wolinella succinogenes.";
RL	Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695(2003).
DR	EMBL; BX571660; CAE10497.1; -.
DR	GO; GO:0016020; C-membrane; IEA.
DR	GO; GO:0005224; F-ATP binding; IEA.
DR	GO; GO:0016301; F-kinase activity; IEA.
DR	GO; GO:000155; F-two-component sensor molecule activity; IEA.
DR	GO; GO:0007165; P-signal transduction; IEA.
DR	InterPro; IPR003594; ATPbind_ATPase.
DR	InterPro; IPR004358; Bact_sens_pr_C.
DR	InterPro; IPR005467; His_kinase.
DR	InterPro; IPR003660; His_kin_HAMP.
DR	InterPro; IPR009082; His_kin_homodim.
DR	Pfam; PF00672; HAMP; 1.
DR	Pfam; PF02518; HATPase_C_1.
DR	PRINTS; PR00344; BCTRLSENSOR.
DR	PROSITE; PS0109; HIS_KIN; 1.
KW	Complete proteome.
SQ	SEQUENCE 548 AA; 63212 MW; D88DB41F238B8BD CRC64;
Query Match	48.0%; Score 59; DB 2; Length 548;
Best Local Similarity	66.7%; Pred. No. 4.4;
Matches 12; Conservative 1; Mismatches 5; Indels 0; Gaps	
QY	6 EVAHREFKDLGEENFKALV 23 :
DB	356 QVKHFQDLTEFTFAQV 373
RESULT 58	
ALBU_NEOFS	
ID_ALBU_NEOFS STANDARD; PRT; 101 AA.	
AC AP3517;	
DT 05-JUL-2004 (Rel. 44, Created)	
DT 05-JUL-2004 (Rel. 44, Last sequence update)	
DT 05-JUL-2004 (Rel. 44, Last annotation update)	
DE Serum albumin (Fragmente).	
OS Neoceratodus forsteri (Australian lungfish).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Dipnoi; Ceratodontiformes; Ceratodontidae; Neoceratodus.	
OX NCBI_TaxID=7892;	
RN [1]	
RP SEQUENCE.	
RC TISSUE=Plasma;	
RA Metcalf V., Brennan S., George P.;	
RT "Using serum albumin to infer vertebrate phylogenies.";	
RL Appl. Bioinformatics 2:597-S107(2003).	
CC -!- FUNCTION: Serum albumin, the main protein of plasma, has a good	
CC binding capacity for water, Ca(2+), Na(+), K(+), fatty acids,	
CC hormones, bilirubin and drugs. Its main function is the regulation	
CC of the colloidal osmotic pressure of blood.	
CC -!- SUBCELLULAR LOCATION: Secreted.	
CC -!- TISSUE SPECIFICITY: Plasma.	
CC -!- SIMILARITY: Belongs to the ALB/AFP/VDB family.	
CC -!- SIMILARITY: Belongs at least 2 albumin domains.	
DR InterPro; IPR000264; Serum albumin.	
DR PROSITE; PS00212; ALBUMIN; PARTIAL.	
KW Copper; Direct protein sequencing; Lipid-binding; Metal-binding;	
FW Repeat.	
FT DOMAIN 1 >80 Albumin 1.	

RT "RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
RN [6]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saichoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK050644; BAC34360.1; -.
DR HSSP; P02768; 1HK1.
DR MGD; MGI:87991; Albi.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR001703; Alphafetoprot.
DR InterPro; IPR000264; Serum albumin.
DR Pfam; PF00273; Serum albumin; 3.
DR PRINTS; PR00803; AFTOPROTEIN.
DR PRINTS; PR00802; SERUMALBUMIN.
DR ProDom; PD002486; Serum albumin; 1.
DR SMART; SM00103; ALBUMIN; 3.
DR PROSITE; PS00212; ALBUMIN; 3.
FT NON TER 1 1
SQ SEQUENCE 576 AA; 65002 MW; F85733E99AE37F04 CRC64;

Query Match 45.5%; Score 56; DB 2; Length 576;

Best Local Similarity 62.5%; Pred. No. 13;

Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 9 HRFKDLGEENFKALVL 24

Db 1 NRYNDLGEQHFGLVL 16

RESULT 40

Q6ZQ53 ID Q6ZQ53 PRELIMINARY; PRT; 569 AA.
AC Q6ZQ53;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE MKIAA0765 protein (Fragment).
GN Name=MKIAA0765;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic tail;
RX PubMed=14621295;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA Kaga Y., Nagase T., Ohara O., Koga H.;
RT "Prediction of the coding sequences of mouse homologues of KIAA gene:
RT cDNAs identified by screening of sequences of 500 mouse KIAA-homologous
RT randomly sampled from size-fractionated libraries."
RL DNA Res. 10:167-180(2003).
DR EMBL; AK129208; BAC98018.1; -.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; RRM_1; 2.
DR SMART; SM00360; RRM; 3.
DR PROSITE; PSS0102; RRM; 2.
FT NON TER 1 1
SQ SEQUENCE 569 AA; 61568 MW; 57480E18D57ED6BA CRC64;

Query Match 43.1%; Score 53; DB 2; Length 569;
Best Local Similarity 56.5%; Pred. No. 35;
Matches 13; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 DAKKSEVAHRFKDLGEENFKALV 23

Db 508 DAKKSEHLHRKKLNGREAFVHIV 530

Search completed: August 19, 2005, 10:55:34
Job time : 58 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 19, 2005, 10:49:44 ; Search time 16 Seconds
(without alignments)

144.325 Million cell updates/sec

Title: US-09-846-328B-1_COPY_2_25

Perfect score: 123

Sequence: 1 DAHKSEVAHRFKDLGEENFKALVL 24

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: Pir1.*
- 2: Pir2.*
- 3: Pir3.*
- 4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	123	100.0	609	1 ABRUS	serum albumin prec
2	110	89.4	600	2 A47391	serum albumin prec
3	108	87.8	607	1 ABBOS	serum albumin prec
4	106	86.2	608	1 ABRTS	serum albumin prec
5	105	85.4	607	1 ABSHS	serum albumin prec
6	100	81.3	607	1 ABHOS	serum albumin prec
7	97	78.9	605	1 ABPGS	serum albumin prec
8	97	78.9	608	2 S57632	serum albumin prec
9	97	78.9	609	2 JC5838	albumin - Mongolia
10	92	74.8	24	2 S29749	serum albumin - do
11	89	72.4	30	2 B61511	serum albumin, mil
12	81	65.9	615	1 ABSCHS	serum albumin prec
13	50	40.7	67	2 T12251	sucrose synthase (
14	50	40.7	384	2 C91051	hypothetical prote
15	50	40.7	384	2 D5028	hypothetical 43.1
16	50	40.7	384	2 A53361	thyroxine-binding
17	49	39.8	153	2 A53361	SAP155 protein - y
18	49	39.8	905	2 S86295	hypothetical prote
19	48	39.0	184	2 T20006	hypothetical prote
20	48	39.0	222	2 A37575	conserved hypotet
21	48	39.0	222	2 A12795	vitamin D-binding
22	48	39.0	474	1 VVHUD	hypothetical prote
23	47.5	38.6	629	2 T06675	probable exported
24	47	38.2	189	2 AB0230	conserved hypotet
25	47	38.2	313	2 E83095	hypothetical prote
26	47	38.2	719	2 F96577	protein F52E1.10 [
27	46.5	37.8	451	2 F89130	hypothetical prote
28	46	37.4	180	2 T44944	hypothetical prote
29	46	37.4	220	2 B72219	ribulose-phosphate

RESULT 1

ABRUS

serum albumin precursor [validated] - human

N;Alternate names: preproalbumin

N;Contains: Kinetensin

C;Species: Homo sapiens (man)

C;Date: 29-Jul-1981 #sequence revision 31-Jan-1997 #text change 09-Jul-2004

C;Accession: A93743; A93936; I39427; I52866; I59313; G01747; S55314; A91420; S06422; S36f

R;Lawn, R.M.; Adelman, J.; Bock, S.C.; Franke, A.E.; Houck, C.M.; Najarian, R.C.; Seeburg

Nucleic Acids Res. 9, 6103-6114, 1981

A;Title: The sequence of human serum albumin cDNA and its expression in Escherichia coli

A;Reference number: A93743; MUID:82081882; PMID:6171778

A;Accession: A93743

A;Molecule type: mRNA

A;Residues: 1-419, 'K', 421-609 <LAW>

A;Cross-references: UNIPROT:P02768; EMBL:V00495; GB:J00078; GB:L00132; GB:L00133; NID:92f

R;Dugalczyk, A.; Law, S.W.; Dennison, O.E.

Proc. Natl. Acad. Sci. U.S.A. 79, 71-75, 1982

A;Title: Nucleotide sequence and the encoded amino acids of human serum albumin mRNA.

A;Reference number: A93936; MUID:82105994; PMID:6275391

A;Accession: A93936

A;Molecule type: mRNA

A;Residues: 1-120, 'G', 122-609 <DUG>

A;Cross-references: EMBL:V00494; NID:928589; PIDN:CAA23753.1; PID:G28590

R;Urano, Y.; Watanabe, K.; Sakai, M.; Tamaoki, T.

J. Biol. Chem. 261, 3244-3251, 1986

A;Title: The human albumin gene. Characterization of the 5' and 3' flanking regions and

A;Reference number: I39427; MUID:86140099; PMID:2419329

A;Accession: I39427

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-26 <URA>

A;Cross-references: GB:M13075; NID:9178330; PIDN:AAAS1688.1; PID:G553173

R;Watkins, S.; Madison, J.; Galliano, M.; Minchiotti, L.; Putnam, F.W.

Proc. Natl. Acad. Sci. U.S.A. 91, 2275-2279, 1994

A;Title: A nucleotide insertion and frameshift cause analbuminemia in an Italian family.

A;Reference number: I59286; MUID:94181575; PMID:8134387

A;Accession: I59286

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 282-290, 'KSRFDLQ' <WAT>

A;Cross-references: GB:S69192; NID:9546032; PIDN:AAAB30282.1; PID:G546033

A;Note: this frame-shift variant, designated albumin Roma, leads to analbuminemia

R;Madison, J.; Galliano, M.; Watkins, S.; Minchiotti, L.; Porta, F.; Rossi, A.; Putnam,

Proc. Natl. Acad. Sci. U.S.A. 91, 6476-6480, 1994

A;Title: Genetic variants of human serum albumin in Italy: point mutants and a carboxyl-

A;Reference number: I59313; MUID:94294404; PMID:8022807

A;Accession: I59313

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 589-590, 'ALPRRVNKLQVQLP' <WAD>

A;Cross-references: GB:S70799; NID:9547231; PIDN:AAAB31177.1; PID:G547232

A;Note: this frame-shift variant is designated albumin Bazzano; four additional variants
R;Menaya, J.; Parrilla, R.; Ayuso, M.S.
submitted to the EMBL Data Library, March 1995
A;Reference number: G08292
A;Accession: G01747
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-120,'G',122-455 <MEN>
A;Cross-references: EMBL:U22961; NID:g763428; PIDN:AAA64922.1; PID:g763431
R;Ledgerwood, E.C.; George, P.M.; Peach, R.J.; Brennan, S.O.
Biochem. J. 308, 321-325, 1995
A;Title: Endoproteolytic processing of recombinant proalbumin variants by the yeast *Kex2*
A;Reference number: S55314; MUID:95275251; PMID:7755581
A;Accession: S55314
A;Molecule type: protein
A;Residues: 19-27 <LED>
R;Meloun, B.; Moravek, L.; Kostka, V.
FEBS Lett. 58, 134-137, 1975
A;Title: Complete amino acid sequence of human serum albumin.
A;Reference number: A91420; MUID:76187907; PMID:1225573
A;Accession: A91420
A;Molecule type: protein
A;Residues: 25-117,'EQ',120-154,'Q',156-193,'E',195-387,'H',389-390,'Y',392-393,'A',395-
A;Reference number: S36882; MUID:93384321; PMID:8373198
A;Accession: S36882
A;Molecule type: protein
A;Residues: 45-67,141-160;311-337;469-490;570-581 <FIN>
R;Kausler, E.; Spitteller, G.
Biol. Chem. Hoppe-Seyler 372, 849-855, 1991
A;Title: Bruchstuecke aus Albumin und beta(2)-Mikroglobulin - Bestandteile der Mittelmol
A;Reference number: S17599; MUID:92126241; PMID:1772598
A;Accession: S17599
A;Molecule type: protein
A;Residues: 25-54;354-357;431-447 <KAU>
A;Note: 49-Leu was also found
R;Carraway, R.E.; Cochran, D.E.; Boucher, W.; Mitra, S.P.
J. Immunol. 143, 1680-1684, 1989
A;Title: Structures of histamine-releasing peptides formed by the action of acid proteas
A;Reference number: A45800; MUID:89341406; PMID:2474609
A;Accession: A45800
A;Molecule type: protein
A;Residues: 166-173,'L' <MOG>
R;Mogard, M.H.; Kobayashi, R.; Chen, C.F.; Lee, T.D.; Reeve Jr., J.R.; Shively, J.E.; Wa
Biochem. Biophys. Res. Commun. 136, 983-988, 1986
A;Title: The amino acid sequence of kinetensin, a novel peptide isolated from pepsin-tre
A;Reference number: A03239; MUID:86242180; PMID:3087352
A;Accession: A03239
A;Molecule type: protein
A;Residues: 166-173,'L' <MOG>
R;Galliano, M.; Minchiotti, L.; Porta, F.; Rossi, A.; Ferri, G.; Madison, J.; Watkins, S
Proc. Natl. Acad. Sci. U.S.A. 87, 8721-8725, 1990
A;Title: Mutations in genetic variants of human serum albumin found in Italy.
A;Reference number: A38255; MUID:91062352; PMID:2247440
A;Accession: A38255
A;Molecule type: protein
A;Residues: 76-111 <GAL1>
A;Accession: B38255
A;Molecule type: protein
A;Residues: 82-105,'K',107-110 <GAL2>
A;Note: this variant is designated albumin Vibo Valentia
A;Accession: A38255
A;Molecule type: protein

A;Residues: 76-83,'K',85-106 <GAL3>
A;Note: this variant is designated albumin Torino
R;Minchiotti, L.; Galliano, M.; Zapponi, M.C.; Tenni, R.
Eur. J. Biochem. 214, 437-444, 1993
A;Title: The structural characterization and bilirubin-binding properties of albumin Heri
A;Reference number: S33298; MUID:93292504; PMID:8513793
A;Accession: S33298
A;Molecule type: protein
A;Residues: 255-263,'E',265-281 <MIN1>
A;Note: this variant is designated albumin Herborn
R;Minchiotti, L.; Galliano, M.; Stoppini, M.; Ferri, G.; Crespeau, H.; Rochu, D.; Porta,
Biochim. Biophys. Acta 1119, 232-238, 1992
A;Title: Two albumins with identical electrophoretic mobility are produced by differ
A;Reference number: S21078; MUID:92190239; PMID:1347703
A;Accession: S21078
A;Molecule type: protein
A;Residues: 354-356,'K',358-378 <MIN2>
A;Note: this variant is designated albumin Sondrio; another variant Paris-2 is reported,
R;He, X.M.; Carter, D.C.
Nature 358, 209-215, 1992
A;Title: Atomic structure and chemistry of human serum albumin.
A;Reference number: A46756; MUID:9233427; PMID:1630489
A;Contents: annotation; X-ray crystallography, 2.8 angstroms
R;Brown, J.R.; Shockley, P.; Behrens, P.Q.
in The Chemistry and Physiology of the Human Plasma Proteins, Bing, D.H., ed., pp.23-40,
A;Reference number: A94442
A;Contents: annotation; three-dimensional structure and disulfide bonds
R;Saber, M.A.; Stockbauer, P.; Moravek, L.; Meloun, B.
Collect. Czech. Chem. Commun. 42, 564-579, 1977
A;Title: Disulfide bonds in human serum albumin.
A;Reference number: A90930
A;Contents: annotation; disulfide bonds
R;Jacobsen, C.
Biochem. J. 171, 453-459, 1978
A;Title: Lysine residue 240 of human serum albumin is involved in high-affinity binding c
A;Reference number: A90299; MUID:78186630; PMID:656055
A;Contents: annotation; bilirubin-binding site
R;Peters, T.; Reed, R.G.
in Albumin: Structure, Biosynthesis, Function, Peters, J., and Sjolholm, I., eds., 11-20,
A;Title: Serum albumin: conformation and active sites.
A;Reference number: A94408
A;Contents: annotation; binding sites
R;Harper, M.E.; Dugaiczky, A.
Am. J. Hum. Genet. 35, 565-572, 1983
A;Title: Linkage of the evolutionarily-related serum albumin and alpha-fetoprotein genes
A;Reference number: A90028; MUID:83279982; PMID:6192711
A;Contents: annotation; gene position
R;Walker, J.E.
FEBS Lett. 66, 173-175, 1976
A;Title: Lysine residue 199 of human serum albumin is modified by acetylsalicylic acid.
A;Reference number: A46755; MUID:76257808; PMID:955075
A;Contents: annotation
A;Note: the nonenzymatic transfer of an acetyl group from aspirin (acetylsalicylic acid)
R;Bohney, J.P.; Fonda, M.L.; Feldhoff, R.C.
FEBS Lett. 298, 266-268, 1992
A;Title: Identification of Lys(190) as the primary binding site for pyridoxal 5'-phosphat
A;Reference number: A56294; MUID:92183881; PMID:1544460
A;Contents: annotation
A;Note: the nonenzymatic binding of pyridoxal phosphate to lysine-214 is described; in p
atase activity
C;Comment: Serum albumin, a predominant protein in the plasma of adults, is synthesized i
lirubin, protoporphyrin, long-chain fatty acids, prostaglandins, steroid hormones (weak t
C;Comment: A large number of variants of human serum albumin have been described.
C;Genetics:
A;Gene: GDB:ALB
A;Cross-references: GDB:118990; OMIM:103600
A;Map position: 4q11-4q13
C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: carrier protein; duplication; metal binding; phosphoprotein; plasma; pyridox
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-24/Domain: propeptide #status experimental <PRO>
F;25-609/Product: serum albumin #status experimental <MPT>
F;29-202/Domain: serum albumin repeat homology <SAL>

P;166-174/Product: kinetensin #status experimental <KIP>
F;221-394/Domain: serum albumin repeat homology <SA2>
F;413-592/Domain: serum albumin repeat homology <SA3>
F;27/Binding site: copper (His) #status predicted
F;77-86,99-115,114-125,148-193,192-201,224-270,269-277,289-303,302-313,340-385,384-393,4
F;214/Binding site: pyridoxal phosphate (lys) (covalent) #status experimental

Query Match 100.0%; Score 123; DB 1; Length 609;
Best Local Similarity 100.0%; Pred. No. 4.7e-10;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDGLGEENFKALVL 24
|||||
Db 25 DAHKSEVAHRFKDGLGEENFKALVL 48
|||||

RESULT 2
A47391
serum albumin precursor - rhesus macaque
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A47391
R;Watkins, S.; Sakamoto, Y.; Madison, J.; Davis, E.; Smith, D.G.; Dwulet, J.; Putnam, P.
Proc. Natl. Acad. Sci. U.S.A. 90, 2409-2413, 1993
A;Title: cDNA and protein sequence of polymorphic macaque albumins that differ in bilirubin binding
A;Reference number: A47391; MUID:93211971; PMID:8460152
A;Contents: B/B homozygote
A;Accession: A47391
A;Status: preliminary
A;Molecule type: mRNA; protein
A;Residues: 1-600 <WAT>
A;Cross-references: UNIPROT:Q28522; GB:M90463; NID:g342294; PIDN:AAA36906.1; PID:g342295
A;Experimental source: liver
A;Note: Sequence extracted from NCBI backbone (NCBIN:128280, NCBI:P:128281)
C;Superfamily: serum albumin; serum albumin repeat homology
F;21-194/Domain: serum albumin repeat homology <SA1>
F;213-386/Domain: serum albumin repeat homology <SA2>
F;405-584/Domain: serum albumin repeat homology <SA3>

Query Match 89.4%; Score 110; DB 2; Length 600;
Best Local Similarity 87.5%; Pred. No. 3.6e-08;
Matches 21; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDGLGEENFKALVL 24
|||||
Db 17 DTHKSEVAHRFKDGLGEHFKGLVL 40
|||||

RESULT 3
ABBS
serum albumin precursor [validated] - bovine
N;Alternate names: 67K protein; preproalbumin
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Apr-1984 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: A38885; A36401; A91258; B60808; S10780; D45800; A26693; A90309; A91458; A94551
R;Holloway, E.W.; Scollenberg, J.K.; Reed, R.G.; Peters Jr., T.
Submitted to the EMBL Data Library, August 1991
A;Description: Bovine serum albumin: cDNA sequence and expression.
A;Reference number: A38885
A;Accession: A38885
A;Molecule type: mRNA
A;Residues: 1-607 <HOL>
A;Cross-references: UNIPROT:P04277; EMBL:M73215
R;Hirayama, K.; Akashi, S.; Furiya, M.; Fukuhara, K.
Biochem. Biophys. Res. Commun. 173, 639-646, 1990
A;Title: Rapid confirmation and revision of the primary structure of bovine serum albumin
A;Reference number: A36401; MUID:91083649; PMID:2260975
A;Accession: A36401
A;Molecule type: protein
A;Residues: 25-41, 'H', 43-189, 'E', 191-213, 'T', 215-323, 'D', 325-393, 'TS', 396-607 <HIR>
Eur. J. Biochem. 98, 477-485, 1979
A;Title: Biosynthesis of bovine plasma proteins in a cell-free system.

A;Reference number: A91258; MUID:80024278; PMID:488109
A;Accession: A91258
A;Molecule type: protein
A;Residues: 1-32 <MAG>
R;Haieh, J.C.; Lin, F.P.; Tam, M.F.
Anal. Biochem. 170, 1-8, 1988
A;Title: Electrophoretic onto glass-fiber filter from an analytical isoelectrofocusing gel
A;Reference number: A60808; MUID:88267456; PMID:3389500
A;Accession: B60808
A;Molecule type: protein
A;Residues: 25-41 <HSI>
R;Strawich, E.; Glimcher, M.J.
Eur. J. Biochem. 191, 47-56, 1990
A;Title: Tooth 'enamelins' identified mainly as serum proteins. Major 'enamelins' is albumin
A;Reference number: S10780; MUID:90336641; PMID:2379503
A;Accession: S10780
A;Molecule type: protein
A;Residues: 25-41, 'H', 43-57, 59-64 <STR>
R;Carraway, R.E.; Cochran, D.E.; Boucher, W.; Mitra, S.P.
J. Immunol. 143, 1680-1684, 1989
A;Title: Structures of histamine-releasing peptides formed by the action of acid proteases
A;Reference number: A45800; MUID:89341406; PMID:2474609
A;Accession: D45800
A;Molecule type: protein
A;Residues: 163-172 <CAR>
R;Carraway, R.E.; Mitra, S.P.; Cochran, D.E.
J. Biol. Chem. 262, 5968-5973, 1987
A;Title: Structure of a biologically active neurotensin-related peptide obtained from pig
A;Reference number: A26693; MUID:87194805; PMID:2437111
A;Accession: A26693
A;Molecule type: protein
A;Residues: 165-172, 'L' <CA2>
R;Reed, R.G.; Putnam, F.W.; Peters Jr., T.
Biochem. J. 191, 867-868, 1980
A;Title: Sequence of residues 400-403 of bovine serum albumin.
A;Reference number: A90309; MUID:82023364; PMID:7283978
A;Accession: A90309
A;Molecule type: protein
A;Residues: 402-433 <REE>
R;Brown, J.R.
Fed. Proc. 34, 591, 1975
A;Title: Structure of bovine serum albumin.
A;Reference number: A91458
A;Accession: A91458
A;Molecule type: protein
A;Residues: 25-41, 'H', 43-117, 'EQ', 120-179, 181-189, 'E', 191-194, 'A', 196-213, 'T', 215-288, 'B',
submitted to the Atlas, April 1975
A;Reference number: A94551
A;Accession: A94551
A;Molecule type: protein
A;Residues: 190-195 <BR2>
R;Brown, J.R.
Fed. Proc. 33, 1389, 1974
A;Reference number: A91457
A;Contents: annotation; disulfide bonds
R;Werlen, R.C.; Offord, R.E.; Rose, K.
Biochem. J. 302, 907-911, 1994
A;Title: Preparation and characterization of novel substrates of insulin proteinase (EC
A;Reference number: S55232; MUID:95031935; PMID:7945219
A;Accession: S55232
A;Status: preliminary
A;Molecule type: protein
A;Residues: 529-536, 569-572 <WER>
C;Superfamily: serum albumin; serum albumin repeat homology
C;Keywords: carrier protein; copper binding; duplication; Plasma
F;1-18/Domain: signal sequence #status experimental <SIG>
F;19-24/Domain: propeptide #status experimental <PRO>
F;25-607/Product: serum albumin #status experimental <MPT>
F;29-201/Domain: serum albumin repeat homology <SA1>
F;220-393/Domain: serum albumin repeat homology <SA2>
F;412-591/Domain: serum albumin repeat homology <SA3>
F;27/Binding site: copper (His) #status predicted

[illegible]

R;Hayaashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and genomic analysis of the verotoxin genes

A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: C91051

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-384 <HAY>

A;Cross-references: UNIPROT:Q8XAA4; GB:BA000007; PID:BA36802.1; PID:gl3362849; GSPDB:G000000001

A;Experimental source: strain O157:H7, substrain RMD 0509952

C;Genetics:

A;Gene: ECs3379

C;Superfamily: conserved hypothetical protein HI0365

Query Match 40.7%; Score 50; DB 2; Length 384;
Best Local Similarity 42.9%; Pred. No. 13;
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGEENFKA 21
| : : : : ||||| : : ||
Db 22 DLNRQMRFPFKDLGKPFRA 42
| : : : : ||||| : : ||

RESULT 16

D65028

A;Title: Hypothetical 43.1 kD protein in ndk-gcpE intergenic region - *Escherichia coli* (strain K-12)

C;Species: *Escherichia coli*

C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

C;Accession: D65028

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of *Escherichia coli* K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: D65028

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-384 <BLAT>

A;Cross-references: UNIPROT:P36979; GB:AE000338; GB:U000096; MUID:gl788862; PID:AA075570.

A;Experimental source: strain K-12, substrain MG1655

C;Genetics:

A;Gene: yfgB

C;Superfamily: conserved hypothetical protein HI0365

Query Match 40.7%; Score 50; DB 2; Length 384;
Best Local Similarity 42.9%; Pred. No. 13;
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGEENFKA 21
| : : : : ||||| : : ||
Db 22 DLNRQMRFPFKDLGKPFRA 42
| : : : : ||||| : : ||

RESULT 17

A53361

A;Title: thyroxine-binding protein, plasma - turtle (*Trachemys scripta*) (fragments)

N;Alternate names: TBP protein

C;Species: *Trachemys scripta* (turtle)

C;Date: 19-Mar-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004

C;Accession: A53361; S41664

R;Licht, P. submitted to the Protein Sequence Database, December 1993

A;Reference number: A53361

A;Accession: A53361

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-30;31-45;46-66;67-74;75-84;85-94;95-109;110-122;123-138;139-153 <LIC>

A;Cross-references: UNIPROT:Q7LZ08

R;Licht, P.; Moore, M.F. Arch. Biochem. Biophys. 309, 47-51, 1994

A;Title: Structure of a reptilian plasma thyroxine binding protein indicates homology to the thyroxine-binding protein of the turtle

A;Reference number: S41664; MUID:94161555; PMID:8117112

A;Accession: S41664

A;Molecule type: protein

A;Residues: 1-30;31-45;46-66;67-74;75-84;85-94;95-109;110-122;123-138;139-153 <LIW>

C;Keywords: plasma

Query Match 39.8%; Score 49; DB 2; Length 153;
Best Local Similarity 33.3%; Pred. No. 7;
Matches 8; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGEENFKALVL 24
| : : : : ||||| : : ||
Db 6 DYVRDKVCFEFLNKGKDFRSLAI 29
| : : : : ||||| : : ||

RESULT 18

S56295

A;Title: SAPI55 protein - yeast (*Saccharomyces cerevisiae*)

N;Alternate names: protein R013; protein YFR040W

C;Species: *Saccharomyces cerevisiae*

C;Date: 02-Sep-1995 #sequence_revision 19-Oct-1995 #text_change 20-Jun-2000

C;Accession: S56295; S62251; S63787

R;Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanuma, S.I. submitted to the EMBL Data Library, May 1995

A;Description: Analysis of the nucleotide sequence of chromosome VI from *Saccharomyces cerevisiae*

A;Reference number: S56186

A;Accession: S56295

A;Molecule type: DNA

A;Residues: 1-905 <MUR>

A;Cross-references: EMBL:D50617; MUID:9836685; PID:g836795; MIPS:YFR040W

R;Murakami, Y. submitted to the EMBL Data Library, December 1994

A;Reference number: S62230

A;Accession: S62251

A;Molecule type: DNA

A;Residues: 1-905 <MOW>

A;Cross-references: EMBL:D44597; MUID:g871938; PID:g871939

R;Eki, T.; Naitou, M.; Hagiwara, H.; Ozawa, M.; Sasanuma, S.I.; Sasanuma, M.; Teuchiya, Y. Yeast 12, 149-167, 1996

A;Title: Analysis of a 36.2 kb DNA sequence including the right telomere of chromosome V

A;Reference number: S63787; MUID:96287652; PMID:8686379

A;Accession: S63787

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-905 <EKI>

A;Cross-references: EMBL:D44597; MUID:g871938; PID:g871939

C;Genetics:

A;Gene: SGD:SAP155

A;Cross-references: SGD:S0001936; MIPS:YFR040W

A;Map position: 6R

Query Match 39.8%; Score 49; DB 2; Length 905;
Best Local Similarity 40.9%; Pred. No. 43;
Matches 9; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 3 HKSEVAHRFKDLGEENFKALVL 24
| : : : : ||||| : : ||
Db 442 HENQLHEKFKPLGFERFKVVEL 463
| : : : : ||||| : : ||

RESULT 19

T20006

A;Title: hypothetical protein C47E12.9 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T20006

R;Coles, L. submitted to the EMBL Data Library, January 1996

A;Reference number: Z19210

A;Accession: T20006

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-184 <WIL>

A;Cross-references: UNIPROT:Q18676; EMBL:Z68882; PID:CAA93103.1; GSPDB:GN00022; CESP:CA4

A;Experimental source: clone C47E12
C;Genetics:
A;Gene: CESP:C47E12.9
A;Map position: 4
A;Introns: 25/3; 51/3; 115/3
C;Superfamily: Caenorhabditis elegans hypothetical protein C47E12.9

Query Match 39.0%; Score 48; DB 2; Length 184;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 HKSEVAHRFKDLGEE 17
| | | | | : | : | : |
Db 149 YSSEVAQKFDLSEE 163

RESULT 20
A97575
hypothetical protein AGR_C_3280 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: A97575
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, P.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: A97575
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-222 <KUR>
A;Cross-references: UNIPROT:Q8UEH3; GB:AE007869; PIDN:AAK87554.1; PID:g15156890; GSPDB:C
C;Genetics:
A;Gene: AGR_C_3280
A;Map position: circular chromosome
C;Superfamily: Neisseria meningitidis probable integral membrane protein NMA2020

Query Match 39.0%; Score 48; DB 2; Length 222;
Best Local Similarity 50.0%; Pred. No. 14;
Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 4 KSEVAHRFKDLGEE 17
| | | | | : | : | : |
Db 151 KGELAHRFNEMGQ 164

RESULT 21
A12795
conserved hypothetical protein Atul784 [imported] - Agrobacterium tumefaciens (strain C5
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: A12795
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: A12795
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-222 <KUR>
A;Cross-references: UNIPROT:Q8UEH3; GB:AB008688; PIDN:AAL42783.1; PID:g17740227; GSPDB:C
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atul784
A;Map position: circular chromosome
C;Superfamily: Neisseria meningitidis probable integral membrane protein NMA2020

Query Match 39.0%; Score 48; DB 2; Length 222;
Best Local Similarity 50.0%; Pred. No. 14;

Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 4 KSEVAHRFKDLGEE 17
| | | | | : | : | : |
Db 151 KGELAHRFNEMGQ 164

RESULT 22
VYHUD
vitamin D-binding protein precursor [validated] - human
A;Alternate names: DBP; Gc-globulin; group-specific component
C;Species: Homo sapiens (man)
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C;Accession: A94076; A46759; A29096; A92765; S39787; A24066; A90427; A03237
R;Yang, F.; Brune, J.L.; Naylor, S.L.; Cupples, R.L.; Naberhaus, K.H.; Bowman, B.H.
Proc. Natl. Acad. Sci. U.S.A. 82, 7994-7998, 1985
A;Title: Human group-specific component (Gc) is a member of the albumin family.
A;Reference number: A94076; MUID:86068030; PMID:2415977
A;Accession: A94076
A;Molecule type: mRNA
A;Residues: 1-474 <YANI>
A;Cross-references: UNIPROT:P02774; GB:X03178; GB:M11321; NID:g31675; PIDN:CAA26938.1; P
A;Experimental source: allele Gc2
R;Witke, W.F.; Gibbs, P.E.M.; Zielinski, R.; Yang, F.; Bowman, B.H.; Dugaiczky, A.
Genomics 16, 751-754, 1993
A;Title: Complete structure of the human Gc gene: differences and similarities between me
A;Reference number: A46759; MUID:93315171; PMID:8325650
A;Accession: A46759
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-431, 'E', '433-435, 'T', '437-474 <WIT>
A;Cross-references: GB:L10641; NID:g340281; PIDN:AAA61704.1; PID:g639896
A;Experimental source: allele Gc1
R;Yang, F.; Naberhaus, K.H.; Adrian, G.S.; Gardella, J.M.; Brissenden, J.E.; Bowman, B.H.
Gene 54, 285-290, 1987
A;Title: The vitamin D-binding protein gene contains conserved nucleotide sequences that
A;Reference number: A29096; MUID:88005794; PMID:2958390
A;Accession: A29096
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-19 <YAN2>
A;Cross-references: GB:M17156; NID:g181489; PIDN:AAA19662.1; PID:g463096
R;Cooke, N.E.; David, E.V.
J. Clin. Invest. 76, 2420-2424, 1985
A;Title: Serum vitamin D-binding protein is a third member of the albumin and alpha fetop
A;Reference number: A92765; MUID:86086396; PMID:2416779
A;Accession: A92765
A;Molecule type: mRNA
A;Residues: 1-167, 'E', '169-326, 'R', '328-431, 'E', '433-435, 'T', '437-474 <COO>
A;Cross-references: GB:M12654; NID:g181481; PIDN:AAA52173.1; PID:g181482
A;Experimental source: allele Gc1
R;Braun, A.; Kofler, A.; Morawietz, S.; Cleve, H.
Biochim. Biophys. Acta 1216, 385-394, 1993
A;Title: Sequence and organization of the human vitamin D-binding protein gene.
A;Reference number: S39787; MUID:94092730; PMID:7505619
A;Accession: S39787
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-431, 'E', '433-435, 'T', '437-474 <BRA>
A;Cross-references: GB:S67480; NID:g455967; PIDN:AAB29423.1; PID:g455970
R;Schoentgen, F.; Metz-Boutigue, M.H.; Jolles, J.; Constans, J.; Jolles, P.
Biochim. Biophys. Acta 871, 189-198, 1986
A;Title: Complete amino acid sequence of human vitamin D-binding protein (group-specific
A;Reference number: A24066; MUID:86216223; PMID:2423133
A;Accession: A24066
A;Molecule type: protein
A;Residues: 17-474 <SCH>
R;Svasti, J.; Kurosky, A.; Bennett, A.; Bowman, B.H.
Biochemistry 18, 1611-1617, 1979
A;Title: Molecular basis for the three major forms of human serum vitamin D binding prote
A;Reference number: A90427; MUID:79145448; PMID:218624
A;Accession: A90427
A;Molecule type: protein

A;Accession: T36873
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-264 <MUR>
A;Cross-references: UNIPROT:Q95230; EMBL:AL109848; PIDN:CAB52834.1; GSPDB:GN00070; SCODEB:SC0E81
A;Experimental source: strain A3(2)
C;Genetics:
C;Superfamily: Streptomyces coelicolor hypothetical protein SCI51.10c

Query Match 36.6%; Score 45; DB 2; Length 264;
Best Local Similarity 52.9%; Pred.No. 47;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 7 VAHRFKDLGSENFKALV 23
| | : ||| : : ||
Db 180 VVARLKELGEASFRVLV 196

RESULT 32
S56055
hypothetical protein YMR241w - yeast (*Saccharomyces cerevisiae*)
N;Alternate names: hypothetical protein YM9408.03
C;Species: *Saccharomyces cerevisiae*
C;Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
R;Accession: S56055
R;Genes: S.; Bowman, S.
submitted to the EMBL Data Library, March 1995
A;Reference number: S56053
A;Accession: S56055
A;Molecule type: DNA
A;Residues: 1-314 <GEN>
A;Cross-references: UNIPROT:Q04013; EMBL:Z48756; NID:g736304; PID:g736307; GSPDB:GN00013
C;Genetics:
A;Gene: SGD:YMR2; MIPS:YMR241w
A;Cross-references: SGD:S0004854
A;Map position: 13R
C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 36.6%; Score 45; DB 2; Length 314;
Best Local Similarity 45.0%; Pred.No. 56;
Matches 9; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 5 SEVAHFRFDLGSENFKALVL 24
| | : ||| ||| : : ||
Db 96 AEAEYRFKSGLNNFASGIL 115

RESULT 33
G64667
NA+/H+ antiporter - *Helicobacter pylori* (strain 26695)
C;Species: *Helicobacter pylori*
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: G64667
R;Tomb, J.F.; Loftus, B.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Lofthouse, R.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.L.; Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpik, P.D.; Smith, H.O.; Fraser, C.; A;Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
A;Reference number: AG4520; MUID:97394467; PMID:9252185
A;Accession: G64667
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-383 <TON>
A;Cross-references: UNIPROT:O25795; GB:AE000624; GB:AE000511; NID:g2314340; PIDN:AAD082222
C;Superfamily: Aquifex aeolicus Na+/H+-exchanging protein napAI

Query Match 36.6%; Score 45; DB 2; Length 383;
Best Local Similarity 53.8%; Pred.No. 69;
Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 HKSEVAHFRFDKLG 15

R; Hughes, J.; Hughes, M.A.
submitted to the EMBL Data Library, January 1994
A; Description: Multiple secondary plant product UDP-glucose glucosyltransferase genes ex
A; Reference number: S41950
A; Accession: S41952
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-394 <HUG>
A; Cross-references: UNIPROT:Q40288; EMBL:X77463; NID:g453250; PID:g453251
C; Superfamily: flavonol O3-glucosyltransferase

Query Match 36.6%; Score 45; DB 2; Length 394;
Best Local Similarity 38.1%; Pred. No. 71;
Matches 8; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 3 HKSEVAHRFKDLGLENFKALV 23
| | | | | : : : : :
Db 353 HHSEIRKRVKEMSDKSKALM 373

RESULT 37
A45565
cysteine proteinase (EC 3.4.22.-) - Theileria annulata
C; Species: Theileria annulata
C; Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C; Accession: A45565
R; Baylis, H.A.; Megson, A.; Mottram, J.C.; Hall, R.
Mol. Biochem. Parasitol. 54, 105-107, 1992
A; Title: Characterisation of a gene for a cysteine protease from Theileria annulata.
A; Reference number: A45565; MUID:92389980; PMID:1518523
A; Accession: A45565
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-441 <BAY>
A; Cross-references: UNIPROT:P25781; GB:M86659; NID:g161886; PID:g161887
A; Experimental source: Hisear
A; Note: sequence extracted from NCBI backbone (NCBIN:112709, NCBIP:112710)
C; Superfamily: papain
C; Keywords: cysteine proteinase; hydrolase
P; 252,381,403/Active site: Cys, His, Asn #status predicted

Query Match 36.6%; Score 45; DB 2; Length 441;
Best Local Similarity 57.1%; Pred. No. 79;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 9 HRFKDLGLENFKAL 22
: : | | | : | | |
Db 165 NKFSDLSDERFKAL 178

RESULT 38
A97208
carbon monoxide dehydrogenase, catalytic chain (coos) [imported] - Clostridium acetobuty
C; Species: Clostridium acetobutylicum
C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 15-Mar-2004
C; Accession: A97208
R; Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J. Bacteriol. 183, 4823-4838, 2001
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cl
A; Reference number: A96900; MUID:21359325; PMID:21359325
A; Accession: A97208
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-639 <KUR>
A; Cross-references: GB:AE001437; PIDN:AAK80452.1; PID:g15025519; GSPDB:GN00168
A; Experimental source: Clostridium acetobutylicum ATCC824
C; Genetics:
A; Gene: CAC2498
C; Superfamily: carbon-monoxide dehydrogenase, beta subunit; hybrid cluster [4Fe-2S-3O] h

Query Match 36.6%; Score 45; DB 2; Length 639;
Best Local Similarity 52.6%; Pred. No. 1.2e+02;

Matches 10; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 2 AHKSEVAHRFKDLGLENFK 20
| | | | | : | | | |
Db 383 AQADETAQRLIELGIENFK 401

RESULT 39
C82860
DNA gyrase subunit B XF0005 [imported] - Xylella fastidiosa (strain 945c)
C; Species: Xylella fastidiosa
C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C; Accession: C82860
R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A; Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A; Reference number: A82515; MUID:20365717; PMID:10910347
A; Note: for a complete list of authors see reference number A59328 below
A; Accession: C82860
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-814 <SIM>
A; Cross-references: UNIPROT:Q9PHD9; GB:AE003855; GB:AE003849; NID:g9104760; PIDN:AAF82818
A; Experimental source: strain 945c
R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; AJ
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carreir, H.
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Praga, J.S.; Franca, S.C.; Franco, M.C.; Frohne
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuraanae, E.E.; Laigre
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.B.; de Sa, R.G.; Santelli, R.V.; Sawasaki
A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Teshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A; Reference number: A59328
A; Contents: annotation
C; Genetics:
A; Gene: XF0005
C; Superfamily: DNA topoisomerase (ATP-hydrolyzing) chain B

Query Match 36.6%; Score 45; DB 2; Length 814;
Best Local Similarity 55.6%; Pred. No. 1.5e+02;
Matches 10; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHRFKDLGLEN 18
| | | | | : | | | |
Db 739 DAKKGRQIQRFKGLGEMN 756

RESULT 40
T18552
saturated Mx1 synthetase A - Myxococcus xanthus
C; Species: Myxococcus xanthus
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C; Accession: T18552
R; Fospiech, A.; Bietenhader, J.; Schupp, T.
Microbiology 142, 741-746, 1996
A; Title: Two multifunctional peptide synthetases and an O-methyltransferase are involved
A; Reference number: Z18967; MUID:97090395; PMID:8936303
A; Accession: T18552
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: DNA
A; Residues: 1-2605 <POS>
A; Cross-references: UNIPROT:Q50858; EMBL:U24657; NID:g1171127; PID:g1171129; PIDN:AAAC4412
C; Genetics:
A; Gene: safa
C; Keywords: carrier protein
P; 535-978/Domain: acetate-CoA ligase homology <AC11>
F; 997-1065/Domain: acyl carrier protein homology <ACP1>
F; 1643-2091/Domain: acetate-CoA ligase homology <ACL2>
F; 2110-2178/Domain: acyl carrier protein homology <ACP2>

Query Match 36.6%; Score 45; DB 2; Length 2605;
Best Local Similarity 46.7%; Pred. No. 4.9e+02;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DAHKSEVAHREPKDLG 15
||| :||| :||
Db 1629 DAHANQLAHLRLQLG 1643

Search completed: August 19, 2005, 10:58:46
Job time : 18 secs

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